

```

Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0
QY 1 M Q N W A T F Q Q K H I I N T P I I C T I M D N N I Y I V G G C K R V N T F I I S S A T T V K A I C T G V I N M N V 60
Ddb 1 M Q N W A T F Q Q K H I I N T P I I C T I M D N N I Y I V G G C K R V N T F I I S S A T T V K A I C T G V I N L N V 60
QY 61 L S T T R F O L N T C T R T S I T P R C P Y S S R T E T N Y I C V K C E N Q Y P V H F A G I G R C P 111
Ddb 61 L S T T R F O L N T C T R T S I T P R C P Y S S R T E T N Y I C V K C E N Q Y P V H F A G I G R C P 111

RESULT 9
US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met(-L) RaCOR1 Met22Leu Met57Leu- (His)6)
US-09-948-391A-22

Query Match 99.0%; Score 601; DB 10; Length 117;
Best Local Similarity 98.2%; Pred. No. 1.2e-60;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0
QY 1 M Q N W A T F Q Q K H I I N T P I I C T I M D N N I Y I V G G C K R V N T F I I S S A T T V K A I C T G V I N M N V 60
Db 7 M Q N W A T F Q Q K H I I N T P I I C T I M D N N I Y I V G G C K R V N T F I I S S A T T V K A I C T G V I N L N V 66
QY 61 L S T T R F O L N T C T R T S I T P R C P Y S S R T E T N Y I C V K C E N Q Y P V H F A G I G R C P 111
Db 67 L S T T R F O L N T C T R T S I T P R C P Y S S R T E T N Y I C V K C E N Q Y P V H F A G I G R C P 117

RESULT 10
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641

```

```

; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

Query Match
Best Local Similarity 99.2%; Score 602; DB 10; Length 111;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
Db 1 MSNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

```

```

RESULT 6
US-09-948-391A-17
; Sequence 17, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; FILE REFERENCE: Recombinant Anti-Tumor RNase
; CURRENT APPLICATION NUMBER: US/09/948,391A
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: (recombinant Met (-1) RacOR1)
US-09-948-391A-17

```

```

Query Match
Best Local Similarity 99.1%; Score 601; DB 10; Length 111;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
Db 1 MGNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

```

```

RESULT 7
US-09-948-391A-21

```

```

; Sequence 21, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; FILE REFERENCE: Recombinant Anti-Tumor RNase
; CURRENT APPLICATION NUMBER: US/09/948,391A
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,
; OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant
; OTHER INFORMATION: Met (-1) RacOR1 Met22Leu Met57Leu)
US-09-948-391A-21

```

```

Query Match
Best Local Similarity 99.0%; Score 601; DB 10; Length 111;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
Db 1 MGNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

```

```

RESULT 8
US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: GOLDBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-21

```

```

Query Match
Best Local Similarity 99.0%; Score 601; DB 10; Length 111;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 2
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15
Query Match 99.2%; Score 602; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.4e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTYKAICTGVINNNVL 61
Db 1 QNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTYKAICTGVINNNVL 60
Qy 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
RESULT 3
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-15

Query Match 99.2%; Score 602; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.4e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTYKAICTGVINNNVL 61
Db 1 QNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTYKAICTGVINNNVL 60
Qy 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
RESULT 4
US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2ser substitution (Met (-1) RaCOR1 Q1S)
US-09-948-391A-26
Query Match 99.2%; Score 602; DB 10; Length 111;
Best Local Similarity 99.1%; Pred. No. 8.5e-61;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MONWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTYKAICTGVINNNV 60
Db 1 MSNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTYKAICTGVINNNV 60
Qy 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
RESULT 5
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 35.6155 Seconds
(without alignments)
865.070 Million cell updates/sec

Title: US-09-961-400-17

Perfect score: 607

Sequence: 1 MNWATFOQKHINTPICN.....ICVKENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	607	100.0	111	10	US-09-961-400-17
2	602	99.2	110	10	US-09-948-391A-15
3	602	99.2	110	10	US-09-961-400-15
4	602	99.2	111	10	US-03-948-391A-26
5	602	99.2	111	10	US-09-961-400-26
6	601	99.0	111	10	US-09-948-391A-17
7	601	99.0	111	10	US-09-948-391A-21
8	601	99.0	111	10	US-09-961-400-21
9	601	99.0	117	10	US-09-948-391A-22
10	601	99.0	117	10	US-09-961-400-22
11	597	98.4	110	10	US-09-948-391A-24
12	597	98.4	110	10	US-09-961-400-24
13	596	98.2	110	10	US-09-961-400-19
14	590	97.2	110	10	US-09-948-391A-19
15	286.5	47.2	105	10	US-09-948-391A-6

16	286.5	47.2	105	10	US-09-961-400-6	Sequence 6, Appli
17	283.5	46.7	111	10	US-09-961-400-9	Sequence 9, Appli
18	282.5	46.5	105	14	US-10-153-882-2	Sequence 2, Appli
19	281.5	46.4	104	10	US-09-961-400-2	Sequence 2, Appli
20	281.5	46.4	105	10	US-09-948-391A-13	Sequence 13, Appli
21	281.5	46.4	105	10	US-09-961-400-13	Sequence 13, Appli
22	281.5	46.4	127	10	US-09-948-391A-28	Sequence 28, Appli
23	281.5	46.4	127	10	US-09-961-400-28	Sequence 28, Appli
24	280.5	46.2	104	10	US-09-948-391A-2	Sequence 2, Appli
25	280.5	46.2	105	10	US-09-961-400-8	Sequence 8, Appli
26	276.5	45.6	104	10	US-09-948-391A-11	Sequence 11, Appli
27	276.5	45.6	104	10	US-09-961-400-11	Sequence 11, Appli
28	275.5	45.4	104	10	US-09-948-391A-4	Sequence 4, Appli
29	275.5	45.4	104	10	US-09-961-400-4	Sequence 4, Appli
30	272.5	44.9	104	9	US-09-986-119-1	Sequence 1, Appli
31	272.5	44.9	104	10	US-09-918-887-1	Sequence 1, Appli
32	271.5	44.7	105	10	US-09-948-391A-8	Sequence 8, Appli
33	271.5	44.7	111	10	US-09-948-391A-9	Sequence 9, Appli
34	269.5	44.4	104	12	US-10-461-713-53	Sequence 53, Appli
35	206	33.9	83	9	US-09-986-119-3	Sequence 3, Appli
36	206	33.9	83	10	US-09-918-887-3	Sequence 3, Appli
37	163	26.9	169	13	US-10-016-447-2	Sequence 2, Appli
38	135.5	22.3	124	12	US-10-037-417-103	Sequence 103, App
39	131.5	21.7	119	12	US-10-016-248-89	Sequence 89, Appli
40	131.5	21.7	119	15	US-10-074-978A-139	Sequence 139, App
41	121	19.9	99	15	US-10-074-978A-141	Sequence 141, App
42	117.5	19.4	124	12	US-10-461-713-52	Sequence 52, Appli
43	117	19.3	147	9	US-09-731-872-254	Sequence 254, App
44	117	19.3	147	10	US-09-876-997-254	Sequence 254, App
45	114.5	18.9	124	9	US-09-981-286A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-17

Query Match 100.0%; Score 607; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNWATFOQKHINTPICNIMDNIIYVGQCKRVNTFISSATTVAICTGVINMV 60
Db 1 MNWATFOQKHINTPICNIMDNIIYVGQCKRVNTFISSATTVAICTGVINMV 60
QY 61 LSTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 111
Db 61 LSTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 111


```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-61

Query Match 45.7%; Score 277.5; DB 3; Length 254;
Best Local Similarity 49.1%; Pred. No. 2.2e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

QY 1 MONWATFOQKHINT-PIICNTIMNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
DB 1 MSDMLTFQKKHITRDVDCDINMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 56
QY 59 NVLSTTRFOLNCTRTSITRPPCYSSRTETNYICVKCENQYVHFAGIGRC 110
DB 57 NVLTISEFYLSDC---NVTSRCKYKLLKSTNKNFCVTCENQAPVHFVGVGSC 105

RESULT 15
US-08-875-811-49
; Sequence 49, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997

;
; COMPUTER READABLE FORM:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-61

Query Match 45.7%; Score 277.5; DB 3; Length 355;
Best Local Similarity 49.1%; Pred. No. 3.3e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

QY 1 MONWATFOQKHINT-PIICNTIMNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
DB 251 MSDMLTFQKKHITRDVDCDINMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 306
QY 59 NVLSTTRFOLNCTRTSITRPPCYSSRTETNYICVKCENQYVHFAGIGRC 110
DB 307 NVLTISEFYLSDC---NVTSRCKYKLLKSTNKNFCVTCENQAPVHFVGVGSC 355

Search completed: May 7, 2004, 21:40:45
Job time : 12.8756 secs
```


QY 59 NVLSTTRFQKHIINT-PIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVI-NM 110
Db 64 NVLTSEFYLSDC---NVTSRPKYKLLKSTNKFVCVTCENQAPVHFVGVGSC 112

RESULT 12

US-08-875-811-63
; Sequence 63, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-63

Query Match 45.7%; Score 277.5; DB 3; Length 129;
Best Local Similarity 49.5%; Pred. No. 9.6e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY 2 QNWATFQKHIINT-PIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVI-NM 59
Db 26 QDWLTFQKXHIINT-PIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVI-NM 81
QY 60 VLSSTTRFQKHIINT-PIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVI-NM 110
Db 82 VLTSEFYLSDC---NVTSRPKYKLLKSTNKFVCVTCENQAPVHFVGVGSC 129

RESULT 13

US-08-875-811-59
; Sequence 59, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-59

Query Match 45.7%; Score 277.5; DB 3; Length 251;
Best Local Similarity 49.1%; Pred. No. 2.2e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;
QY 1 MQNWATFQKHIINT-PIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVI-NM 58
Db 147 MSDWLTFFQKXHIINT-PIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVI-NM 202
QY 59 NVLSTTRFQKHIINT-PIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVI-NM 110
Db 203 NVLTSEFYLSDC---NVTSRPKYKLLKSTNKFVCVTCENQAPVHFVGVGSC 251

RESULT 14

US-08-875-811-61
; Sequence 61, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

```
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ran, David B.
; REGISTRATION NUMBER: 38,589
; REFERENCE/DOCKET NUMBER: 15280-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-626-288-1

Query Match      45.7%; Score 277.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 7.4e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWAFFQOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 59
Db 1 QDWLTFQKKHITNTDRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

QY 60 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 57 VLTTFSEYLSDC---NVTSRPCKYKLNKSTNKFVCVTENQAPVHFVGVGSC 104

RESULT 10
US-09-095-429-1
; Sequence 1, Application US/09095429
; Patent No. 6649393
; GENERAL INFORMATION:
; APPLICANT: Youle, Richard
; APPLICANT: Vasandani, Veena
; APPLICANT: Wu, Yon-Neng
; APPLICANT: Boix, Ester
; APPLICANT: Argelt, Wojetech
; TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
; TITLE OF INVENTION: Allows Production by Recombinant Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,429
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,288
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ran, David B.
; REGISTRATION NUMBER: 38,589
; REFERENCE/DOCKET NUMBER: 15280-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
```

```
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-095-429-1

Query Match      45.7%; Score 277.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 7.4e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWAFFQOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 59
Db 1 QDWLTFQKKHITNTDRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

QY 60 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 57 VLTTFSEYLSDC---NVTSRPCKYKLNKSTNKFVCVTENQAPVHFVGVGSC 104
```

```
RESULT 11
US-08-875-811-32
; Sequence 32, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02568
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-32
```

```
Query Match      45.7%; Score 277.5; DB 3; Length 112;
Best Local Similarity 49.1%; Pred. No. 8.1e-25;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

QY 1 QNWAFFQOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 8 MSDWLTFFQKHITNTDRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 63
```

APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-51

Query Match 46.0%; Score 279.5; DB 3; Length 358;
Best Local Similarity 49.1%; Pred. No. 2e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
Qy 1 MNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MEDWLTFOQKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 56

Qy 59 NVLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 VLTTFSEFYLSDC---NVTSPCKYKLLKSTNKFVCVCENQAPVHFVGVGSC 105

RESULT 7
US-09-394-268-1
Sequence 1, Application US/09394268
Patent No. 6175003
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF MAKING THEM
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-394-268-1
Query Match 45.7%; Score 277.5; DB 3; Length 104;

Best Local Similarity 49.5%; Pred. No. 7.4e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
Qy 2 QNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59
Db 1 QDWLTFQKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56
Qy 60 VLSSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 VLTTFSEFYLSDC---NVTSPCKYKLLKSTNKFVCVCENQAPVHFVGVGSC 104

RESULT 8
US-09-687-748-1
Sequence 1, Application US/09687748
Patent No. 6423515
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US 01
CURRENT APPLICATION NUMBER: US/09/687,748
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: 09/394,268
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-687-748-1

Query Match 45.7%; Score 277.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 7.4e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 2 QNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NMN 59
Db 1 QDWLTFQKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

Qy 60 VLSSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 VLTTFSEFYLSDC---NVTSPCKYKLLKSTNKFVCVCENQAPVHFVGVGSC 104

RESULT 9
US-08-626-288-1
Sequence 1, Application US/08626288
Patent No. 6649392
GENERAL INFORMATION:
APPLICANT: Youle, Richard
APPLICANT: Vasandani, Veena
APPLICANT: Wu, Yon-Neng
APPLICANT: Boix, Ester
APPLICANT: Ardelet, Wojciech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which Allows Production by Recombinant Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,288
FILING DATE: No. 6649392 yet assigned

```
DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match
Best Local Similarity 46.9%; Score 284.5; DB 1; Length 104;
Matches 55; Conservative 16; Mismatches 31; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 59
Db 1 EDMLTFQKHITNTRDVCNINMSTNLF----HCKDKNTFIYSRPEPVKAICKGIISK 56

QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKENQYVHFAGIGRC 110
Db 57 VLITSEFYLSDC---NVTSPCKYKLLKSTNKFCTVCENQAPVHFVGVGSC 104

RESULT 4
US-08-875-811-39
; Sequence 39, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; OPERATING SYSTEM: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-39

Query Match
Best Local Similarity 46.0%; Score 279.5; DB 3; Length 105;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 EDMLTFQKHITNTRDVCNINMSTNLF----HCKDKNTFIYSRPEPVKAICKGIISK 56

QY 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKENQYVHFAGIGRC 110
```

```
Db 57 NVLITSEFYLSDC---NVTSPCKYKLLKSTNKFCTVCENQAPVHFVGVGSC 105

RESULT 5
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; OPERATING SYSTEM: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-41

Query Match
Best Local Similarity 46.0%; Score 279.5; DB 3; Length 355;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 251 MEDWLTFOQKHITNTRDVCNINMSTNLF----HCKDKNTFIYSRPEPVKAICKGIISK 306

QY 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKENQYVHFAGIGRC 110
Db 307 NVLITSEFYLSDC---NVTSPCKYKLLKSTNKFCTVCENQAPVHFVGVGSC 355

RESULT 6
US-08-875-811-51
; Sequence 51, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
```

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..111
OTHER INFORMATION: /note= "Frog Lectin from Rana
catesbeiana"
US-08-891-848-12

Query Match 97.0%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 6.6e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
OTHER INFORMATION: /note= "Frog Lectin from Rana
catesbeiana"
US-08-891-848-12

QY 2 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVINMV 60
:|||||
Db 1 ENWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVINMV 60
:|||||

QY 61 LSTTRFQLNCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
:|||||
Db 61 LSTTRFQLNCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
:|||||

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..111

OTHER INFORMATION: /note= "Frog Lectin from Rana
catesbeiana"
US-08-875-811-8

Query Match 97.0%; Score 588.5; DB 3; Length 111;
Best Local Similarity 98.2%; Pred. No. 6.6e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
OTHER INFORMATION: /note= "Frog Lectin from Rana
catesbeiana"
US-08-891-848-12

QY 2 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVINMV 60
:|||||
Db 1 ENWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVINMV 60
:|||||

QY 61 LSTTRFQLNCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
:|||||
Db 61 LSTTRFQLNCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
:|||||

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5007 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:28:45 ; Search time 12.8756 Seconds
(without alignments)
445.066 Million cell updates/sec

Title: US-09-961-400-17
Perfect score: 607
Sequence: 1 MQNWATFOQKHINTPICN.....ICVKENQYDPVHEAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	97.0	111	2	US-08-891-848-12
2	588.5	97.0	111	3	US-08-875-811-8
3	284.5	46.9	104	1	US-08-467-955-2
4	279.5	46.0	105	3	US-08-875-811-39
5	279.5	46.0	355	3	US-08-875-811-41
6	279.5	46.0	358	3	US-08-875-811-51
7	277.5	45.7	104	3	US-09-394-268-1
8	277.5	45.7	104	4	US-09-687-748-1
9	277.5	45.7	104	4	US-09-687-748-1
10	277.5	45.7	104	4	US-09-095-429-1
11	277.5	45.7	112	3	US-08-875-811-32
12	277.5	45.7	129	3	US-08-875-811-63
13	277.5	45.7	251	3	US-08-875-811-59
14	277.5	45.7	254	3	US-08-875-811-61
15	277.5	45.7	355	3	US-08-875-811-49
16	277.5	45.7	355	3	US-08-875-811-57
17	277.5	45.7	355	3	US-08-875-811-64
18	277.5	45.7	366	3	US-08-875-811-55
19	277.5	45.7	379	3	US-08-875-811-43
20	274.5	45.2	104	1	US-08-283-971-1
21	274.5	45.2	104	1	US-07-921-619-1
22	274.5	45.2	104	1	US-08-467-955-1
23	274.5	45.2	104	2	US-08-891-848-13
24	272.5	44.9	104	3	US-08-875-811-1
25	272.5	44.9	104	3	US-09-394-268-2
26	272.5	44.9	104	4	US-09-071-672-1
27	272.5	44.9	104	4	US-09-687-748-2

28 272.5 44.9 104 4 US-09-986-119-1 Sequence 1, Appli

29 272.5 44.9 105 3 US-08-875-811-26 Sequence 26, Appl

30 272.5 44.9 106 3 US-08-875-811-28 Sequence 28, Appl

31 272.5 44.9 107 3 US-08-875-811-30 Sequence 30, Appl

32 271.5 44.7 105 3 US-08-875-811-24 Sequence 24, Appl

33 269.5 44.4 104 4 US-08-626-288-2 Sequence 2, Appli

34 269.5 44.4 104 4 US-09-095-429-2 Sequence 2, Appli

35 268.5 44.2 358 3 US-08-875-811-45 Sequence 45, Appl

36 268.5 44.2 365 3 US-08-875-811-20 Sequence 20, Appl

37 250.5 41.3 107 3 US-08-875-811-22 Sequence 22, Appli

38 239.5 39.5 111 3 US-08-875-811-47 Sequence 47, Appl

39 236 38.9 114 3 US-09-223-118-3 Sequence 2, Appli

40 232.5 38.3 360 3 US-08-875-811-47 Sequence 47, Appl

41 227 37.4 114 3 US-09-223-118-2 Sequence 2, Appli

42 226 37.2 114 3 US-09-223-118-1 Sequence 1, Appli

43 225 37.1 114 3 US-09-223-118-4 Sequence 4, Appli

44 206 33.9 83 3 US-08-875-811-2 Sequence 2, Appli

45 206 33.9 83 4 US-09-071-672-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-891-848-12

; Sequence 12, Application US/08891848

; Patent No. 5955073

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Youle, Richard J.

; APPLICANT: Newton, Dianne L.

; APPLICANT: Nicholls, Peter J.

; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/891,848

; FILING DATE: No. 5955073 yet assigned

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/125,462

; FILING DATE: 22-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/014,082

; FILING DATE: 04-FEB-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/779,195

; FILING DATE: 22-OCT-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/510,696

; FILING DATE: 20-APR-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 015280-110310US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 111 amino acids

; TYPE: amino acid

XX AC AAY28865;
 XX DT 25-JAN-2000 (first entry)
 XX DE Rana pipiens liver ribonuclease (RaPLR1).
 XX DE Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;
 XX KW ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
 XX KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;
 XX KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
 XX OS Rana pipiens.
 XX PN WO9950398-A2.
 XX PD 07-OCT-1999.
 XX PF 26-MAR-1999; 99WO-US006641.
 XX PR 27-MAR-1998; 98US-0079751P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Rybak SM, Newton DL;
 XX DR WPI; 1999-610847/52.
 XX DR N-PSDB; AAZ08124.
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
 XX FT treating cancers, viral infections or autoimmune diseases.
 XX PS Claim 1; Page 55; 71pp; English.
 XX CC The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.
 XX CC Carboxy terminal end of RaPLR1 has a covalently bound ligand binding
 XX CC moiety, which can be a LL2 antibody directed against CD22 on cancerous B
 XX CC cells or human chorionic gonadotrophin (hCG) effective against Kaposi's
 XX CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
 XX CC without an N-terminal methionine due to the presence of a signal peptide
 XX CC that is cleaved by bacteria. The soluble expression of ribonuclease
 XX CC allows the proteins to be fused in-frame with ligand binding moieties to
 XX CC form cytotoxic fusion proteins. They can be used for treatment of cancer
 XX CC and autoimmune diseases
 XX SQ Sequence 104 AA;
 Query Match 46.4%; Score 281.5; DB 2; Length 104;
 Best Local Similarity 49.5%; Pred. No. 2.9e-24;
 Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
 QY 2 QNWATFOOKHLINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVAICTGVI-NWN 59
 Db 1 QDWLTFQKKHLNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGHIASKN 56
 QY 60 VLSTTRFQLTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC 110
 Db 57 VLTITSEFYLSDC--NVTISRECKYKLKSTNTFCVTCENQAPVHFVGVC 104
 RESULT 13
 AAY28871
 ID AAY28871 standard; protein; 105 AA.
 XX AC AAY28871;
 XX DT 25-JAN-2000 (first entry)
 XX DE Recombinant Met (-1) RaPLR1 Gln1Ser amino acid sequence.
 XX KW Recombinant Met (-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22;
 XX KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 XX KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;

KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
 KW autoimmune disease; RNase.
 XX OS Rana pipiens.
 XX OS Synthetic.
 XX FT Key Location/Qualifiers
 XX FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"
 XX FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"
 XX PN WO9950398-A2.
 XX PD 07-OCT-1999.
 XX PF 26-MAR-1999; 99WO-US006641.
 XX PR 27-MAR-1998; 98US-0079751P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Rybak SM, Newton DL;
 XX DR WPI; 1999-610847/52.
 XX DR N-PSDB; AAZ08129.
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
 XX FT treating cancers, viral infections or autoimmune diseases.
 XX PS Claim 34; Page 61; 71pp; English.
 XX CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
 XX CC protein with Met at position 1 and Gln2Ser. Carboxy terminal end of
 XX CC recombinant RaPLR1 has a covalently bound ligand binding moiety, which
 XX CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 XX CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
 XX CC Recombinant ribonucleases can be expressed in bacteria without an N-
 XX CC terminal methionine due to the presence of a signal peptide that is
 XX CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 XX CC proteins to be fused in-frame with ligand binding moieties to form
 XX CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 XX CC autoimmune diseases
 XX SQ Sequence 105 AA;
 Query Match 46.4%; Score 281.5; DB 2; Length 105;
 Best Local Similarity 49.1%; Pred. No. 3e-24;
 Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;
 QY 1 MQNWATFOOKHLINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVAICTGVI-NM 58
 Db 1 MSDWLTFOKKHLNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGHIASK 56
 QY 59 NVLSTTRFQLTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC 110
 Db 57 NVLITSEFYLSDC--NVTISRECKYKLKSTNTFCVTCENQAPVHFVGVC 105
 RESULT 14
 AAY28879
 ID AAY28879 standard; protein; 127 AA.
 XX AC AAY28879;
 XX DT 25-JAN-2000 (first entry)
 XX DE Rana pipiens Clone 5a1b ribonuclease.
 XX KW Rana pipiens ribonuclease Clone 5a1b; RaPLR1; covalently bound; RNase;
 XX KW LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
 XX KW Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer;
 XX KW recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;

```

ID AAY28869 standard; protein; 105 AA.
XX
AC AAY28869;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
XX
KW Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1;
XX CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase;
XX KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;
XX KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
XX KW cancer; frog; autoimmune disease.
XX
OS Rana pipiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Met not found in wild type RaPLR1"
FT Misc-difference 1
FT /note= "(His)6 histidine tag attached to N-terminal Met"
FT Misc-difference 24
FT /note= "wild type Met replaced with Leu"
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08127.
XX
XX New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 4; Page 59; 7lpp; English.
XX
CC The present sequence is a recombinant Rana pipiens ribonuclease protein
CC (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu
CC Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand
CC binding moiety, which can be a LL2 antibody directed against CD22 on
CC cancerous B cells or human chorionic gonadotropin (hCG) effective
CC against Kaposi's sarcoma cells. Recombinant ribonucleases can be
CC expressed in bacteria without an N-terminal methionine due to the
CC presence of a signal peptide that is cleaved by bacteria. The soluble
CC expression of ribonuclease allows the proteins to be fused in-frame with
CC ligand binding moieties to form cytotoxic fusion proteins. They can be
CC used for treatment of cancer and autoimmune diseases
XX
SQ Sequence 105 AA;
Query Match 46.7%; Score 283.5; DB 2; Length 105;
Best Local Similarity 49.1%; Pred.No.1.7e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
QY 1 MQNATFOOKHIINT-PIICNTIMDNIIYVGQCKRVNTFIISATTVKACTGVI-NM 58
DB 1 MQDLTFQKHLINTRDVCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGLIASK 56
QY 59 NVLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCNQVPVHFAGIGRC 110
DB 57 NVLTSEFYLSDC---NVTSRPCYKYLKSKTNTFCVTCENQAPVHFVGVC 105
RESULT 11
AAY28865
ID AAY28865 standard; protein; 104 AA.
AAY39400
ID AAY39400 standard; protein; 105 AA.
XX
AC AAY39400;
XX
DT 01-DEC-1999 (first entry)
XX
DE Recombinant frog Onconase.
XX
KW Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.
XX
OS Rana pipiens.
XX
PN WO9946389-A1.
XX
PD 16-SEP-1999.
XX
PF 11-MAR-1999; 99WO-US004252.
XX
PR 11-MAR-1998; 98US-0077557P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen H, Leung S;
XX
DR WPI; 1999-551416/46.
DR N-PSDB; AAZ19767.
XX
XX A new recombinant Onconase used to treat, e.g. colon cancer.
PT
PS Example 1; Fig 1; 42pp; English.
XX
CC This sequence represents recombinant frog Onconase. Onconase has
CC ribonuclease and anti-tumour activity. The cDNA was produced via PCR
CC (using primers AAZ19768-Z19769) of two synthetic DNAs whose sequences
CC encoded most of the N-terminal or the C-terminal amino acids of mature
CC Onconase. The two PCR products generated encoded either the N-terminal 54
CC amino acids (minus the initial methionine) or the C-terminal 51 amino
CC acids, and were ligated in frame at an NruI site. The cDNA was then
CC subcloned into a vector e.g., pBluescript, where the ATG initiation codon
CC was ligated to the cDNA. After expression in E. coli, the recombinant
CC protein was purified. The initial N-formyl methionine was cleaved off and
CC the now N-terminal glutamate residue cyclised to form an N-terminal
CC pyroglutamate. The pyroglutamate residue forms part of the phosphate
CC binding pocket of Onconase and is essential for both ribonuclease and anti-
CC tumour activity. Onconase is a 12 kD ribonuclease which causes cell
CC death as a result of potent inhibition of protein synthesis by a
CC mechanism involving inactivation of cellular RNA. It is not inhibited by
CC mammalian placental ribonuclease inhibitor, which may explain its
CC enhanced cytotoxicity relative to mammalian enzymes. It has anti-tumour
CC activity against a variety of solid tumours e.g. colon or pancreatic
CC cancers, and can be used alone or in combination with other anti-cancer
CC agents such as tamoxifen. When used as an anti-tumour agent, Onconase can
CC be conjugated to a marker which targets it to a specific cell type
XX
SQ Sequence 105 AA;
Query Match 46.5%; Score 282.5; DB 2; Length 105;
Best Local Similarity 50.0%; Pred.No.2.3e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY 1 MQNATFOOKHIINT-PIICNTIMDNIIYVGQCKRVNTFIISATTVKACTGVI-NM 58
DB 1 MQDLTFQKHIINTKTDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGLIASK 56
QY 59 NVLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCNQVPVHFAGIGRC 110
DB 57 NVLTSEFYLSDC---NVTSRPCYKYLKSKTNTFCVTCENQAPVHFVGVC 105
RESULT 12
AAY28865
ID AAY28865 standard; protein; 104 AA.

```


SQ Sequence 110 AA;

Query Match 98.4%; Score 597; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2.3e-60;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWAIFQOKHIIINTPIICNTIMDNIIYIVGGQCKRVNTFIISATTVKAICTGVINMNVLS 62
 DB 2 NWAIFQOKHIIINTPIICNTIMDNIIYIVGGQCKRVNTFIISATTVKAICTGVINMNVLS 61

QY 63 TTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 111
 DB 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 110

RESULT 6
 AAY28874
 ID AAY28874 standard; protein; 110 AA.
 XX
 AC AAY28874;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
 KW Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;
 KW RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; bullfrog; RNase; autoimmune disease.
 XX
 OS Rana catesbeiana.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 22 /note= "Wild type Met replaced with Leu"
 FT FT
 FT Misc-difference 57 /note= "Wild type Met replaced with Leu"
 FT FT
 XX WO9950398-A2.
 XX
 XX 07-OCT-1999.
 XX
 XX 26-MAR-1999; 99WO-US006641.
 XX
 XX 27-MAR-1998; 98US-0079751P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Rybak SM, Newton DL;
 XX
 XX WPI; 1999-610847/52.
 XX
 XX N-PSDB; AAZ08132.
 XX
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 XX treating cancers, viral infections or autoimmune diseases.
 XX
 XX Claim 22; Page 64; 71pp; English.
 XX
 XX The present sequence is a recombinant Rana catesbeiana oocyte
 XX ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
 XX end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
 XX which can be a LL2 antibody directed against CD22 on cancerous B cells or
 XX human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma
 XX cells. Recombinant ribonucleases can be expressed in bacteria without an
 XX N-terminal methionine due to the presence of a signal peptide that is
 XX cleaved by bacteria. The soluble expression of ribonuclease allows the
 XX proteins to be fused in-frame with ligand binding moieties to form
 XX cytotoxic fusion proteins. They can be used for treatment of cancer and
 XX autoimmune diseases
 XX
 XX Sequence 110 AA;

Query Match 98.2%; Score 596; DB 2; Length 110;
 Best Local Similarity 98.2%; Pred. No. 3e-60;
 Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFOQKHIIINTPIICNTIMDNIIYIVGGQCKRVNTFIISATTVKAICTGVINMNVLS 61
 DB 1 QNWATFOQKHIIINTPIICNTILDNIIYIVGGQCKRVNTFIISATTVKAICTGVINMNVLS 60

QY 62 STRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 111
 DB 61 STRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 110

RESULT 7
 AAY33321
 ID AAY33321 standard; protein; 111 AA.
 XX
 AC AAY33321;
 XX
 DT 29-NOV-1999 (first entry)
 XX
 DE Frog lectin protein fragment.
 XX
 KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
 KW heavy chain; cell surface marker; treatment; tumor; viral infection;
 KW parasite infection; immune dysfunctional cell; autoimmune disease;
 KW contraceptive; cell separation; transplantation; bone marrow ablation;
 KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
 XX
 OS Rana catesbeiana.
 XX
 XX US5955073-A.
 XX
 XX 21-SEP-1999.
 XX
 XX 09-JUL-1997; 97US-00891848.
 XX
 XX 20-APR-1990; 90US-00510696.
 XX
 XX 22-OCT-1991; 91US-00779195.
 XX
 XX 04-FEB-1993; 93US-00014082.
 XX
 XX 22-SEP-1993; 93US-00125462.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Rybak SM, Newton DL, Nicholls PJ, Youle RJ;
 XX
 XX WPI; 1999-560488/47.
 XX
 XX Recombinantly fused pancreatic RNase-targeting proteins useful for
 XX treating tumors, infections, immune or autoimmune disorders and as a
 XX contraceptive.
 XX
 XX Example 3; Fig 19; 47pp; English.
 XX
 XX This invention describes a novel nucleic acid construct comprising
 XX sequences encoding functional pancreatic RNase and a second protein
 XX (preferably the light and heavy chains of an antibody) which binds a
 XX specific cell surface marker on a target cell and functions as a
 XX cytotoxic agent. The products can be used for selectively killing cells
 XX expressing a specific surface marker. They can be used for treating
 XX tumors or infected cells (e.g. cells infected by viruses (especially
 XX latent or chronic virus infections, such as human immunodeficiency virus
 XX (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and
 XX II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster,
 XX cytomegalovirus) and cells infected with parasites (such as the malaria
 XX parasite)). They can also be used for treating immune dysfunctional cells
 XX in immune and autoimmune diseases. Additionally, they may be used as
 XX contraceptives. Finally they can also be used for cell separation in
 XX vitro by selectively killing unwanted types of cells (e.g. in bone
 XX marrow) prior to transplantation into a patient undergoing marrow
 XX ablation by radiation or for killing leukemia cells or T-cells that would
 XX cause graft-versus-host disease. This sequence represents a bullfrog

Query Match 99.2%; Score 602; DB 2; Length 111;
 Best Local Similarity 99.1%; Pred. No. 6.2e-61;
 Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
 DB 1 MSNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNTCTRTSITPRPCPSYRSRTETNYICVKENQYVPHFAGIGRCP 111
 DB 61 LSTTRFQNTCTRTSITPRPCPSYRSRTETNYICVKENQYVPHFAGIGRCP 111

RESULT 4
 AAY28876
 ID AAY28876 standard; protein; 111 AA.
 XX
 AC AAY28876;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant Met (-1) RaCOR1 Met22Leu Met57Leu- (His)6 protein.
 XX
 KW Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu- (His)6; RaCOR1;
 KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; bullfrog; RNase; autoimmune disease.
 XX
 OS Rana catesbeiana.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
 FT Misc-difference 23 /note= "Wild type Met replaced with Leu"
 FT Misc-difference 58 /note= "Wild type Met replaced with Leu"
 XX
 FN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US006641.
 XX
 PR 27-MAR-1998; 98US-0079751P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL;
 XX
 DR WPI; 1999-610847/52.
 DR N-PSDB; AAZ08133.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 XX
 PS Claim 22; Page 66; 71pp; English.
 XX
 CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6
 CC tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1
 CC has a covalently bound ligand binding moiety, which can be a LL2 antibody
 CC directed against CD22 on cancerous B cells or human chorionic
 CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion

CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases
 XX
 SQ Sequence 111 AA;
 Query Match 99.0%; Score 601; DB 2; Length 111;
 Best Local Similarity 98.2%; Pred. No. 8.1e-61;
 Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
 DB 1 MQNWATFOQKHIIINTPIICNTILNDNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNTCTRTSITPRPCPSYRSRTETNYICVKENQYVPHFAGIGRCP 111
 DB 61 LSTTRFQNTCTRTSITPRPCPSYRSRTETNYICVKENQYVPHFAGIGRCP 111

RESULT 5
 AAY28877
 ID AAY28877 standard; protein; 110 AA.
 XX
 AC AAY28877;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant RaCOR1 Gln1Ser amino acid sequence.
 XX
 KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; autoimmune disease.
 XX
 OS Rana catesbeiana.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"
 FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"
 XX
 FN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US006641.
 XX
 PR 27-MAR-1998; 98US-0079751P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL;
 XX
 DR WPI; 1999-610847/52.
 DR N-PSDB; AAZ08134.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 XX
 PS Claim 22; Page 67; 71pp; English.
 XX
 CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of
 CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
 CC Recombinant ribonucleases can be expressed in bacteria without an N-
 CC terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX
 SQ Sequence 111 AA;
 Query Match 100.0%; Score 607; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.7e-61;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQWATFQQRKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATVKAICTGVINNV 60
 DB 1 MQWATFQQRKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATVKAICTGVINNV 60
 QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111
 DB 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111
 RESULT 2
 AAY28872
 ID AAY28872 standard; protein; 110 AA.
 XX
 AC AAY28872;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
 XX
 KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
 KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
 KW human chorionic gonadotropin; hCG; recombinant ribonuclease; bullfrog;
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
 KW RNase.
 XX
 OS Rana catesbeiana.
 OS Synthetic.
 XX
 FN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US006641.
 XX
 PR 27-MAR-1998; 98US-0079751P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL;
 XX
 DR WPI; 1999-610847/52.
 DR N-PSDB; AAZ08130.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 XX
 PS Claim 22; Page 62; 71pp; English.
 XX
 CC The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
 CC protein encoded by a cDNA modified for expression in E. coli. Carboxy
 CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotropin (hCG) effective against Kaposi's Sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX

SQ Sequence 110 AA;
 Query Match 99.2%; Score 602; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.1e-61;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QNWATFQQRKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATVKAICTGVINNV 61
 DB 1 QNWATFQQRKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATVKAICTGVINNV 60
 QY 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111
 DB 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110
 RESULT 3
 AAY28878
 ID AAY28878 standard; protein; 111 AA.
 XX
 AC AAY28878;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant Met (-1) RaCOR1 Gln1Ser amino acid sequence.
 XX
 KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
 KW CD22; RNase; autoimmune disease.
 XX
 OS Rana catesbeiana.
 OS Synthetic.
 XX
 FN Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"
 XX
 FN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US006641.
 XX
 PR 27-MAR-1998; 98US-0079751P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL;
 XX
 DR WPI; 1999-610847/52.
 DR N-PSDB; AAZ08135.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 XX
 PS Claim 22; Page 68; 71pp; English.
 XX
 CC The present sequence is a recombinant Rana catesbeiana ribonuclease
 CC (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end
 CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 CC chorionic gonadotropin (hCG) effective against Kaposi's sarcoma cells.
 CC Recombinant ribonucleases can be expressed in bacteria without an N-
 CC terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX
 SQ Sequence 111 AA;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:25:55 ; Search time 47.3489 Seconds
(without alignments)
662.376 Million cell updates/sec

Title: US-09-961-400-17
Perfect score: 607
Sequence: 1 MQNWATFOQKHIIPTIICN.....ICVKCENQYFVHFGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	607	100.0	111	2	AAY28873
2	602	99.2	110	2	AAY28872
3	602	99.2	111	2	AAY28878
4	601	99.0	111	2	AAY28876
5	597	98.4	110	2	AAY28877
6	596	98.2	110	2	AAY28874
7	588.5	97.0	111	2	AAY33321
8	286.5	47.2	105	2	AAY28867
9	284.5	46.9	104	2	AAY28864
10	283.5	46.7	105	2	AAY28869
11	282.5	46.5	105	2	AAY39400
12	281.5	46.4	104	2	AAY28865
13	281.5	46.4	105	2	AAY28871
14	281.5	46.4	127	2	AAY28879
15	279.5	46.0	105	2	AAY35123
16	279.5	46.0	355	2	AAY35125
17	279.5	46.0	358	2	AAY35130
18	278.5	45.9	104	2	AAY28866
19	277.5	45.7	104	2	AAY30301
20	277.5	45.7	104	4	AAB31666
21	277.5	45.7	104	5	ABG32650
22	277.5	45.7	112	2	ABG32650 Northern
23	277.5	45.7	251	2	AAY35118 R. pipien
24	277.5	45.7	251	2	AAY35134 R. pipien
25	277.5	45.7	355	2	AAY35135 R. pipien
26	277.5	45.7	355	2	AAY35133 R. pipien

26	277.5	45.7	355	2	AAW35129	R. pipien
27	277.5	45.7	366	2	AAW35132	R. pipien
28	277.5	45.7	379	2	AAW35126	R. pipien
29	276.5	45.6	104	2	AAY28870	Recombina
30	274.5	45.2	104	2	AAR12344	Protein w
31	274.5	45.2	104	2	AAR47303	ONCONASE
32	274.5	45.2	104	2	AAW00736	Protein d
33	274.5	45.2	104	2	AAW14065	Onconase
34	274.5	45.2	104	2	AAW06543	Antitumou
35	274.5	45.2	104	2	AAW88233	Rana pipi
36	274.5	45.2	104	2	AAY33322	Frog onco
37	272.5	44.9	104	4	ABG31667	Amino aci
38	272.5	44.9	104	5	ABG31617	Northern
39	272.5	44.9	105	2	AAW35116	R. pipien
40	272.5	44.9	106	2	AAW35122	R. pipien
41	272.5	44.9	107	2	AAW35117	R. pipien
42	271.5	44.7	104	2	AAW30302	Recombina
43	271.5	44.7	105	2	AAW35115	R. pipien
44	268.5	44.2	358	2	AAW35127	R. pipien
45	268.5	44.2	365	2	AAW35131	R. pipien

ALIGNMENTS

RESULT 1

AAY28873
ID AAY28873 standard; protein; 111 AA.

XX AC AAY28873;

XX 25-JAN-2000 (first entry)

XX Recombinant Met (-1) RaCOR1.

XX Recombinant Met (-1) RaCOR1.

KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW RNase; autoimmune disease.

XX Rana catesbeiana.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1

FT /note= "Met not found in wild type RaCOR1"

XX WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US0006641.

XX 27-MAR-1998; 98US-0079751P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Rybak SM, Newton DL;

DR WPI; 1999-610847/52.

XX N-PSDB; AA208131.

PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 63; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte

XX ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal

XX end of recombinant RaCOR1 has a covalently bound ligand binding moiety,

XX which can be a LL2 antibody directed against CD22 on cancerous B cells, or

XX human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma


```

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE.
RC TISSUE=Milk, and Serum;
RX MEDLINE=97409980; PubMed=9266695;
RA Strydom D.J., Bond M.D., Vallee B.L.;
RT "An angiogenic protein from bovine serum and milk -- purification and
RL Eur. J. Biochem. 247:535-544 (1997).
CC -!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and
CC has very low ribonuclease activity. Has potent angiogenic
CC activity. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs.
CC -!- TISSUE SPECIFICITY: Serum and milk.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR HSP; P10152; IAGI.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Glycoprotein;
KW Pyroliodone carboxylic acid.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 39 39 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
FT DISULFID 25 80
FT DISULFID 38 91
FT DISULFID 56 106
FT CARBOHYD 33 33 N-LINKED (GLCNAC...).
SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 21.2%; Score 127.5; DB 1; Length 123;
Best Local Similarity 30.6%; Pred. No. 7e-07;
Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5;

QY 6 FQKHINTPI-----ICNTIMDNNIYVGGCKRVNTFISSATTVKAIC---TGVINM 57
Db 8 FLKHYDPSPTGHDDRYCINTWERR--NMTPCKDTWTFIHGSDDIRAVCDRNGEPYR 65

QY 58 NVLSTTR--FQNTCTRTSITPR-PCPYSSRTETNYICVKENQYPVH 102
Db 66 NGLRRSRPFQVTCRRHGGSPRPFCRYAFRANRVIVIRCDGDFPIH 113

RESULT 14
RNBR GIRCA STANDARD; PRT; 141 AA.
AC Q29542; Q29533;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN BRN.
OS Giraffa camelopardalis (Giraffe).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
OC Giraffidae; Giraffa.
OX NCBI_TaxID=9894;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96139017; PubMed=8587129;
RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
RT species.";
RL J. Mol. Evol. 41:850-858 (1995).

```

```

[2]
RN SEQUENCE OF 31-114 FROM N.A.
RP MEDLINE=93367815; PubMed=8360916;
RA Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
RA Carsana A., Palmieri M., Furia A.;
RT "Sequences related to the ox pancreatic ribonuclease coding region in
RL J. Mol. Evol. 37:29-35 (1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S81743; AAB36137.1; -
DR EMBL; S65126; AAB27931.1; -
DR HSP; P00656; 2RNS.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT ACT_SITE 41 41 BY SIMILARITY.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC... (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 141 AA; 15592 MW; 73745EFE9079591F CRC64;

Query Match 21.2%; Score 127.5; DB 1; Length 141;
Best Local Similarity 30.6%; Pred. No. 8.1e-07;
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

QY 4 ATFOQKH-----INTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINM 57
Db 6 AKFRQHMDSGSSSSNSVNCQMKRR-RMTGRCCKPVNTFVHESLADVKVCS---QK 61

QY 58 NVL-----STTRFQNTCTRTSITPR-CPYSSRTETNYICVKE-NOY-PVHFA 104
Db 62 NITCKNGQPCYQSNSTMTITDCRETGSSKYPNCAYKTSQKYITVACEGPNYPVPHFD 121

QY 105 G 105
Db 122 G 122

RESULT 15
RNBR AXIPR STANDARD; PRT; 151 AA.
AC P87350;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN BRN.
OS Axis porcinus (Hog deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Axis.
OX NCBI_TaxID=57737;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=98278842; PubMed=9611269;
RA Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,

```

[illegible]

16-OCT-2001 (Rel. 40, Last annotation update)
RN. Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9203604; PubMed=1754384;
RA Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
RA Viola M., Palmieri M., Russo E., Furia A.;
RT "Molecular cloning of the gene encoding the bovine brain ribonuclease
and its expression in different regions of the brain.";
RL Nucleic Acids Res. 19:6469-6474 (1991).
RN [2]
RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
RC TISSUE=Brain;
RX MEDLINE=89214015; PubMed=3243767;
RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
RA Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bovine brain.";
RL J. Biochem. 104:939-945 (1988).
RN [3]
RP SEQUENCE OF 27-167 FROM N.A.
RX MEDLINE=96139017; PubMed=8587129;
RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
species.";
RL J. Mol. Evol. 41:850-858 (1995).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sb-sib.ch).
CC
CC
CC EMBL; X59767; CAA2439.1; -;
CC EMBL; S81744; AAB36138.1; -;
CC PIR; S20066; S20066.
CC HSP; P00656; 2RNS.
CC GlycoSuiteDB; P39873; -;
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; rnaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNase_Pc; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC Hydroxylase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 167 RIBONUCLEASE, BRAIN.
FT ACT_SITE 38 38 BY SIMILARITY.
FT ACT_SITE 67 67 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 52 110 BY SIMILARITY.
FT DISULFID 66 121 BY SIMILARITY.
FT DISULFID 84 136 BY SIMILARITY.
FT DISULFID 91 98 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .).
FT CARBOHYD 155 155 O-LINKED.
FT CARBOHYD 159 159 O-LINKED.
FT CONFLICT 155 155 T -> S (IN REF. 2).
SQ SEQUENCE 167 AA; 18450 MW; 681CAAC3CC2FC459 CRC64;
Query Match 22.2%; Score 133.5; DB 1; Length 167;
Best Local Similarity 31.4%; Pred. No. 2.1e-07;

Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;
QY 4 ATFOQKH;------INTPLICNTMDNNIYVGGCKRVNTFISSATTVAICTGVNM 57
DB 32 AKFRQHMDSGSSSSSNPNQNMKRR-RMTHGCKPNTFVHESLDDVKAACS---QK 87
QY 58 NVL-----STTRFQLNTCTRTSTTPRP-CPYSSRTETNYTCVKE-NQY-PVHFA 104
DB 88 NITCKNGHPCVQSKSTMSITDCRETGSGSKYPNCAKYTSQKQYITVACGPNYPVHFD 147
QY 105 G 105
DB 148 G 148
RESULT 10
RNP_PIG STANDARD; PRT; 124 AA.
ID AC P00671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASEI OR RNSI.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=70104197; PubMed=5460946;
RA Jackson R.L., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. II. The
amino acid sequence of the reduced S-aminoethylated protein.";
RL J. Biol. Chem. 245:637-653 (1970).
RN [2]
RP REVISION TO 2.
RA Wierenga R.K., Huizinga J.D., Gastra W., Welling G.W., Beintema J.J.;
RT "Affinity chromatography of porcine pancreatic ribonuclease and
reinvestigation of the N-terminal amino acid sequence.";
RL FEBS Lett. 31:181-185 (1973).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=70104198; PubMed=4904878;
RA Phelan J.J., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. 3. The
disulfide bonds.";
RL J. Biol. Chem. 245:654-661 (1970).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; A92071; NREG.
DR HSP; P00656; 1SRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .).

```

DR PTR; A00818; NRWHK.
DR HSP; P00656; LSRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 76 76 N-LINKED (GLCNAC...) (30%).
SQ SEQUENCE 124 AA; 14125 MW; F57475459F697E20 CRC64;

Query Match 22.5%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 9.7e-08;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 6 EQQKHII-----NTPICNTIMNNIYVGGCKRNTFTIISATVTKAICTGVINMNV 59
Db 8 FQHQHDSGNSGPNPNYCNQMMRR--KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63
QY 60 L-----SSTRFQNTCTRTSITPR-CPYSSNTFTNYICVKE-NQY-PVHF 103
Db 64 LCKNGRTNCYESNTWHITDCRTGSKYPNCAKTSQKEKHIVACEGPNYPVPHF 120

RESULT 8
ANGI_MOUSE
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=91025023; PubMed=2222458;
RX Bond M.D., Vallee B.L.;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rata S.S., Loquellano N.A., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length

```

```

human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP PARTIAL SEQUENCE.
RX TISSUE=Serum;
RA MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -1- FUNCTION: May function as a tRNA-specific ribonuclease that binds
to actin on the surface of endothelial cells; once bound,
angiogenin is endocytosed and translocated to the nucleus, thereby
promoting the endothelial invasiveness necessary for blood vessel
formation. Angiogenin induces vascularization of normal and
malignant tissues. Abolishes protein synthesis by specifically
hydrolyzing cellular tRNAs.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; U22516; AAA91366.1; -
DR EMBL; BC055355; AH55355.1; -
DR PIR; A35932; A35932.
DR HSP; P03950; 1A4Y.
DR MGD; MGI:88022; Ang.
DR InterPro; IPR001427; RNaseA.
DR PRINTS; PR00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145 ANGIOENIN.
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16228 MW; 06944260B764938 CRC64;

Query Match 22.5%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 1.1e-07;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 33 CKRVNTFTIISATVTKAIC--TGVINMNV-LSTTRFQNTCTRTSITPR-PCPYSSRTE 87
Db 63 CKDVTFTHGKSNKAIKANGSPYRENRMSKSPFQVTKTGGSFPPPCQYRASAG 122
QY 88 TNYICVKCNQYVPHF 103
Db 123 FRHVVIACENGLPVHF 138

RESULT 9
RNER_BOVIN
ID RNER_BOVIN STANDARD; PRT; 167 AA.
AC P39873;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

```

```

RT RT fibroblasts."
RL Mol. Cell. Biol. 17:1503-1512(1997).
CC -!- FUNCTION: Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs (By similarity).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U72672; AAC05794.1; -.
DR HSSP; P10152; IAGI.
DR MGD; MGI:1201793; Angl.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00032; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
FT DISULFID 81 130
SQ SEQUENCE 145 AA; 16696 MW; DE9D3BC92FD682C CRC64;

Query Match 25.7%; Score 154.5; DB 1; Length 145;
Best Local Similarity 43.6%; Pred. No. 1e-09; Indels 9; Gaps 4;
Matches 34; Conservative 12; Mismatches 23;

QY 33 CKRVNTFTIISATTVKAIC-----TGVINNVLSLTFQMLTCTRTSITPR-PCPYSSR 85
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
D6 63 CKRVNTFTIHTKNIKAICGNGREYGV-NFRI-SNSRFQVTTCTHKGSPPPCQYNAF 120
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 86 TETNYICVKCENQYPVHF 103
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D6 121 KDFRYIVIACEDGWPVHF 138

RESULT 6
ANGR_MOUSE
ID ANGR_MOUSE STANDARD; PRT; 145 AA.
AC Q6438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-related protein precursor.
CN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Nobile V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RT protein gene and two pseudogenes.";
RL Genomics 29:200-206(1995).

```

```

CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U22519; AAA91367.1; -.
DR HSSP; P03950; IAA4.
DR MGD; MGI:104984; Angpr.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00032; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal; Hydrolase; Nuclease; Endonuclease;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
FT DISULFID 81 130
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4D CRC64;

Query Match 24.8%; Score 149.5; DB 1; Length 145;
Best Local Similarity 43.4%; Pred. No. 3.6e-09; Indels 5; Gaps 3;
Matches 33; Conservative 10; Mismatches 28;

QY 33 CKRVNTFTIISATTVKAIC---TGVINNV-LSTTRFQMLTCTRTSITPR-PCPYSSRTE 87
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
D6 63 CKRVNTFTIHTKNIKAICGKGSFYGNLRISKRQVTTCTHKGRSPRPPCYRASKG 122
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 88 TNYICVKCENQYPVHF 103
||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
D6 123 FRYIIIGCENGWPVHF 138

RESULT 7
RNP_BALAC
ID RNP_BALAC STANDARD; PRT; 124 AA.
AC P00673;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
CN RNASE1 OR RNS1.
OS Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Balaenoptera.
OX NCBI_TaxID=9767;
RN [1]
RP SEQUENCE.
RX MEDLINE=76277855; PubMed=962870;
RA Emmens M., Welling G.W., Beintema J.J.;
RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
RT ribonuclease.";
RL Biochem. J. 157:317-323(1976).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphogluconolactides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

```

RL J. Biochem. 106:729-735(1989).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; JX0085; JX0085.
DR HSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Pyrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT DISULFID 34 82 BY SIMILARITY.
FT DISULFID 52 97 BY SIMILARITY.
FT DISULFID 94 111 PROBABLE.
SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 62.1%; Score 374; DB 1; Length 111;
Best Local Similarity 65.8%; Pred. No. 2.1e-33;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

Qy 1 QNWATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NMN 58
Db 1 QNWAKFEKHIRSTSIDCNTIMDKAIYVGGCKKERTFISSDNDVKAICSGVSPDK 60

Qy 59 VLSITRFOLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 61 ELSITSFKINTCIRDSITPRCPYHPSPDNNKICVKCKQLPVHFGVIGKC 111

RESULT 4
RN30_RANPI STANDARD; PRT; 104 AA.
ID RN30_RANPI
AC P22069;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P-30 protein (EC 3.1.27.-) (Onconase).
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=91093131; PubMed=1985896;
RA Ardelit W., Mikulski S.M., Shogen K.;
RT "Amino acid sequence of an anti-tumor protein from Rana pipiens
RT oocytes and early embryos. Homology to pancreatic ribonucleases.";
RL J. Biol. Chem. 266:245-251(1991).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=93066156; PubMed=1438177;
RA Mosimann S.C., Johns K.L., Ardelit W., Mikulski S.M., Shogen K.,
RA James M.N.G.;
RT "Comparative molecular modeling and crystallization of P-30 protein:
RT a novel antitumor protein of Rana pipiens oocytes and early
RT embryos.";
RL Proteins 14:392-400(1992).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=94166079; PubMed=8120892;
RA Mosimann S.C., Ardelit W., James M.N.G.;
RT "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an
RT amphibian ribonuclease with anti-tumor activity.";
RL J. Mol. Biol. 236:1141-1153(1994).

CC -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity
CC against several tumor cell lines in vitro, as well as antitumor
CC in vivo. It exhibits a ribonuclease-like activity against high
CC molecular weight ribosomal RNA.
CC -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PDB; 1ONC; 31-JAN-94.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW Pyrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT ACT_SITE 10 10
FT ACT_SITE 31 31
FT ACT_SITE 97 97
FT DISULFID 19 68
FT DISULFID 30 75
FT DISULFID 48 90
FT DISULFID 87 104
FT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT TURN 33 38
FT STRAND 41 45
FT HELIX 46 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 46.1%; Score 277.5; DB 1; Length 104;
Best Local Similarity 49.5%; Pred. No. 4.5e-23;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NMN 58
Db 1 QDWLTFQKKHITNTRDVCNIMTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56

Qy 59 VLSITRFOLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTFSEFVLSDC--NVTSRPCKYKLLKSTNKKFCVTCENQAPVHFVGVGSC 104

RESULT 5
ANG3_MOUSE STANDARD; PRT; 145 AA.
ID ANG3_MOUSE
AC P97802;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
DE (EF-5).
GN ANG3 OR ANGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RX MEDLINE=97184476; PubMed=9032278;
RA Fu X., Kamps M.P.;
RT "E2a-Pbx1 induces aberrant expression of tissue-specific and


```

CC residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)
CC as substrates, and prefers the former. The S-lectins in frog eggs
CC may be involved in the fertilization and development of the frog
CC embryo. This lectin agglutinates various animal cells, including
CC normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC human origin. It is cytotoxic against several tumor cells.
CC
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF039104; AAD10702.1; -.
CC PIR; A27121; A27121.
CC PDB; 1BC4; 28-OCT-98.
CC PDB; 1M07; 21-JAN-03.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; RNaseA; 1.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNaseA; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
CC Signal; Pyrrolidone carboxylic acid.
CC SIGNAL 1 22
CC FT CHAIN 23 133 RIBONUCLEASE, OOCYTES.
CC FT MOD RES 23 23 PYRROLIDONE CARBOXYLIC ACID.
CC FT ACT_SITE 32 32
CC FT ACT_SITE 57 57
CC FT ACT_SITE 125 125
CC FT DISULFID 41 93
CC FT DISULFID 56 103
CC FT DISULFID 74 118
CC FT DISULFID 115 132
CC FT HELIX 25 32
CC FT HELIX 41 45
CC FT TURN 48 49
CC FT STRAND 59 63
CC FT HELIX 67 73
CC FT TURN 74 74
CC FT STRAND 79 84
CC FT STRAND 90 95
CC FT STRAND 105 110
CC FT STRAND 114 119
CC FT TURN 120 121
CC FT STRAND 122 129
CC FT STRAND 133 AA; A7D62594F7D16F0C CRC64;
CC
CC Query Match 98.3%; Score 591.5; DB 1; Length 133;
CC Best Local Similarity 99.1%; Pred. No. 1.1e-56;
CC Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
CC
CC QY 1 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMV 59
CC Db 23 QNWATFOQKHINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMV 82
CC
CC QY 60 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 110
CC Db 83 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGRCP 133
CC
CC RESULT 2
CC LECS_RANJA
CC ID LECS_RANJA STANDARD; PRT; 111 AA.
CC AC P18839;
CC DT 01-NOV-1990 (Rel. 16, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

```

DE Sialic acid-binding lectin (EC 3.1.1.27.-).
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Iitani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs.";
RL J. Biochem. 108:139-143(1990).
CC -!- FUNCTION: The S-lectins in frog eggs may be involved in the
CC fertilization and development of the frog embryo. This lectin
CC preferentially agglutinates a large variety of tumor cells, but it
CC does not agglutinate non-transformed cells and erythrocytes.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC PIR; JX0120; JX0120.
DR HSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
FT SEQUENCE 111 AA; 12326 MW; FDBBDDF3834ED679 CRC64;
CC
CC Query Match 75.6%; Score 455; DB 1; Length 111;
CC Best Local Similarity 78.4%; Pred. No. 4.1e-42;
CC Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;
CC
CC QY 1 QNWATFOQKHINTP-IICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGV-INNM 58
CC Db 1 QNWAFQEKHIPNTSINCNTIMDKSIYVGGQCKRVNTFISSATTVKAICSGASTRN 60
CC
CC QY 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKENQYPVHFAGIGR 109
CC Db 61 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKENRPLVHFAGIGR 111
CC
CC RESULT 3
CC RNPL_RANJA
CC ID RNPL_RANJA STANDARD; PRT; 111 AA.
CC AC P14626;
CC DT 01-APR-1990 (Rel. 14, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Ribonuclease, liver (EC 3.1.1.27.5).
CC OS Rana catesbeiana (Bull frog).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90130374; PubMed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT liver.";

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.55659 Seconds

(without alignments)
1030.796 Million cell updates/sec

Title: US-09-961-400-15

Perfect score: 602

Sequence: 1 QNWATFOQKHIIPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591.5	98.3	133	1	RNPO_RANCA
2	455	75.6	111	1	LECS_RANCA
3	374	62.1	111	1	RNPL_RANCA
4	277.5	46.1	104	1	RN30_RANPI
5	154.5	25.7	145	1	ANG3_MOUSE
6	149.5	24.8	145	1	ANGR_MOUSE
7	135.5	22.5	124	1	RNP_BALAC
8	135.5	22.5	145	1	ANGI_MOUSE
9	133.5	22.0	167	1	RNBR_BOVIN
10	132.5	22.0	124	1	RNP_PIG
11	131.5	21.8	119	1	RNP_IGUIG
12	128.5	21.3	151	1	RNBR_CAPCA
13	127.5	21.2	123	1	ANG2_BOVIN
14	127.5	21.2	141	1	RNBR_GIRCA
15	127.5	21.2	151	1	RNBR_AXIPR
16	125	20.8	146	1	ANGI_SAIISC
17	124	20.6	146	1	ANGI_MIOTA
18	123.5	20.5	143	1	RNBR_SHEEP
19	122.5	20.3	124	1	RNP_ANTAM
20	122.5	20.3	146	1	ANGI_CERAE
21	122	20.3	122	1	RNP_MACRU
22	120.5	20.0	128	1	RNP_MYOOC
23	120.5	20.0	149	1	RNP_MOUSE
24	120	19.9	146	1	ANGI_AOTTR
25	120	19.9	147	1	ANGI_PONPY
26	119.5	19.9	123	1	ANGI_PIG
27	118.5	19.7	128	1	RNPF_CAVO
28	118	19.6	146	1	ANGI_SAGOE
29	117.5	19.5	128	1	RNP_HORSE
30	116.5	19.4	124	1	RNP_CAMDR
31	116.5	19.4	128	1	RNP_PROGU
32	115.5	19.2	119	1	RNS4_BOVIN
33	115.5	19.2	146	1	ANGI_MACMU

34	114	18.9	148	1	ANGI_BOVIN
35	113.5	18.9	124	1	RNP_RANTA
36	113.5	18.9	146	1	ANGI_PAPHA
37	113	18.8	147	1	ANGI_HUMAN
38	113	18.8	147	1	ANGI_PANTR
39	112.5	18.7	124	1	RNP_CAPCA
40	112.5	18.7	124	1	RNP_GIRCA
41	112.5	18.7	148	1	RNS4_MOUSE
42	112	18.6	125	1	ANGI_RABIT
43	111.5	18.5	130	1	ANGI_CRILLO
44	111.5	18.5	147	1	RNS4_RAT
45	111.5	18.5	149	1	RNP_ACOCA

ALIGNMENTS

RESULT 1
RNPO_RANCA STANDARD; PRT; 133 AA.
AC P11916; Q9PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
DE binding lectin) (SBL-C).
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease. Tissue distribution, cloning, purification, cytotoxicity, and active residues for RNase activity.";
RT J. Biol. Chem. 273:6395-6401(1998).
RL [2]
RP SEQUENCE OF 23-133.
RX TISSUE=Egg;
RA MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kawada M., Nitta K., Sakakibara F., Kawauchi H., Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [4]
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=848385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H., Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
RN [5]
RP STRUCTURE BY NMR OF 23-133.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

P10152	bos taurus
P00666	rangifer ta
Q8wn64	papio hamad
P03950	homo sapien
Q8wme8	pan troglod
P00664	capreolus c
P00662	giraffa cam
Q9jjhl	mus musculu
P31347	oryctolagus
E24717	cricetulus
O55004	rattus norv
Q9wtt5	acomys cahi

```
QY 33 CKEVNTFISSATVKAICTG-----VINNVLSLSTRFQNLCTRTSITPR-PCPYSSRTE 87
Db 39 CKEVNTFIHGTRNDIKAIKNDKNGEPYNNFRSKSPFQITTCXKKGSGNPPCGYRATAG 98
QY 88 TNYICVKCENQYFVHF 103
Db 99 FRTIACENGLPVHF 114

RESULT 15
NRGPB
pancreatic ribonuclease (EC 3.1.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gastra, W.; Beintema, J.J.
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID:77185023; PMID:862624
A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 <VAN>
A;Note: 64-pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein, hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 19.7%; Score 118.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 8.5e-05;
Matches 37; Conservative 14; Mismatches 43; Indels 23; Gaps 6;

QY 6 FQQRHI-----INTPIICNTIMDNIIYVGQCKRVNTFISSATVKAICTGVINNV 59
Db 8 FQRQMDPEGSPSSNVCNVMIR-NMTQGRCKPVNTFVHESLADYQAVC---FQKNV 63
QY 60 L-----STTRFQNLCTRTSITPR-CPYSSRTETNYICVKCENQ--YFVHF 103
Db 64 LCKNGQTNICYQSYGRMRITDCRVTSSTSSKFPNCSYRMSQAKSIIVACEGDPYFVHF 120
```

Search completed: May 7, 2004, 21:54:55
Job time : 10.9813 secs


```
Db 6 AKFERQHIDSNPSSVSSNYCNQMMKSR-NLTQGRCKPVNTFFVHESLADVQAVCS---QK 61
Qy 58 NVL-----STTRFQLNCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHF 103
Db 62 NVACKNGQTCYQSYSTMSITDCRETGSSKYPENCAKTKTQAKKHIIIVACEGNPYVPVHY 120

RESULT 11
NRKGR
pancreatic ribonuclease (EC 3.1.1.27.5) - red kangaroo
N;Alternate names: RNase 1; RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833
R;Gaastera, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
A;Accession: A00833
A;Molecule type: protein
A;Status: preliminary
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 20.3%; Score 122; DB 1; Length 122;
Best Local Similarity 30.7%; Pred. No. 3.6e-05;
Matches 35; Conservative 16; Mismatches 45; Indels 18; Gaps 6;

Qy 6 FQOKHI-----INTPIICNTIMNNIYVGGCKRVNTFISSATTVKAIC----- 51
Db 7 FQOKHI-----INTPIICNTIMNNIYVGGCKRVNTFISSATTVKAIC----- 51
Qy 52 TGVNNMLSTTRFQLNCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHF 103
Db 66 NGRNCTC-YKSNLSLITNCRGASKYPCNQVETSNLNQLIIVACEGQYVPVHF 118

RESULT 12
NRUC
pancreatic ribonuclease (EC 3.1.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00822
A;Molecule type: protein
A;Residues: 1-128 <VAN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;13,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 20.0%; Score 120.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 5.4e-05;
Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;

Qy 6 FQOKHI-----INTPIICNTIMNNIYVGGCKRVNTFISSATTVKAICTGVINNV 59
Db 8 FERQHMDSRGSPSTNPYCNEMKSR-NMTQGRCKPVNTFFVHESLADVQAVC---FQKNV 63
Qy 60 L-----STTRFQLNCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHF 103
Db 64 LCKNGQTCYQSYSTMSITDCRETGSSKYPENCAKTKTQAKKHIIIVACEGNPYVPVHF 120
```

RESULT 13

NRMS

```
pancreatic ribonuclease (EC 3.1.1.27.5) precursor - mouse
N;Alternate names: RNase 1; RNase A
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: A34090; S22598; A00830
R;Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A;Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A;Reference number: A34090; MUID:90136034; PMID:2299980
A;Accession: A34090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <SCH>
A;Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific
A;Reference number: S22598; MUID:92107684; PMID:1840677
A;Accession: S22598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <SAM>
A;Cross-references: EMBL:X60103; NID:g53981; PIDN:CRA42697.1; PID:g53982
R;lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A;Title: The amino acid sequence of mouse pancreatic ribonuclease.
A;Reference number: A00830; MUID:80024269; PMID:556267
A;Accession: A00830
A;Molecule type: protein
A;Residues: 26-149 <LEN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F;37,66,144/Active site: His, Lys, His #status predicted
F;51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F;62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.0%; Score 120.5; DB 1; Length 149;
Best Local Similarity 30.8%; Pred. No. 6.3e-05;
Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

Qy 6 FQOKHI-----INTPIICNTIMNNIYVGGCKRVNTFISSATTVKAICTGVINNV 59
Db 33 FQOKHMDPGSSINSPTYCNQMKRR-DMTGSKCPVNTFFVHESLADVQAVCS---QENV 88
Qy 60 L-----STTRFQLNCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHF 103
Db 89 TCKNRKSNCKYSSSALHTDCHLKGNSKYPNCYDKTQYQKHIIIVACEGNPYVPVHF 145

RESULT 14
A43825
angiotensin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29834; A43825
R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiotensins: discernme
A;Reference number: S29833; MUID:93192291; PMID:8448182
A;Accession: S29834
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <BN>
A;Note: this sequence was submitted to the Protein Sequence Database, December 1992
C;Superfamily: pancreatic ribonuclease

Query Match 19.9%; Score 119.5; DB 1; Length 123;
Best Local Similarity 39.5%; Pred. No. 6.5e-05;
Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;
```

Molecule type: protein
Residues: 27-154, 'S', 156-166 <WAT>
Experimental source: brain
Superfamily: pancreatic ribonuclease
Keywords: glycoprotein; hydrolase
38,67,145/Active site: His, Lys, His #status predicted
52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted
88/Binding site: carboxylate (Asn) (covalent) #status experimental
155/Binding site: carbohydrate (Thr) (covalent) #status experimental
159/Binding site: carbohydrate (Ser) (covalent) #status experimental
Query Match 22.2%; Score 133.5; DB 2; Length 167;
Best Local Similarity 31.4%; Pred. No. 3.6e-06;
Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;

RESULT 8
NRPG
pancreatic ribonuclease (EC 3.1.27.5) - pig
N:Alternate names: RNase A
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 24-Apr-1984 sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A92071; A91391; A00816
R:Jackson, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A:Title: The primary structure of porcine pancreatic ribonuclease. II. The
A:Accession number: A92071; MUID:70104197; PMID:5460946

A:Accession: A92071
A:Molecule type: protein
A:Residues: 1,'Q',3-124 <JAC>
R:R.Wierenga, R.K.; Huijinga, J.D.; Gaastra, W.; Wellling, G.W.; Beintema, J.J.
P:FEBS Lett. 31, 181-185, 1973
A:Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
A:Reference number: A91391
A:Accession: A91391
A:Molecule type: protein
A:Residues: 1-124 <WIE>
R:Phelan, J.J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A:Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bonds
A:Reference number: A92072; MUID:70104198; PMID:4904878
A:Contents: annotation; disulfide bonds
A:Supersfamily: pancreatic ribonuclease

RESULT 9
S4111 pancreatic ribonuclease - common iguana
C:Species: Iguana iguana (common iguana)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C:Accession: S4111
R:Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A>Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A:Reference number: S4111; MUID:94139745; PMID:8307028

A;Accession: S41111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease

```

Query Match      21.8%; Score 131.5; DB 2; Length 119;
Best Local Similarity 30.4%; Pred. No. 4e-06;
Matches 35; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

1 QNWATFOQKHI-----INTPLICNTMDNNIYIVGGCKRVNTFLISSATTVKAIC-- 51
  |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
1 QDWSSFKQKHIDYDETSASNNAYCDLWMQRR--NLNPTKCKTRNTFVHASSEIQOVCGS 59
  |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

52 --TGVINMNVLSITRFQLNTCTRSIT--PRCPYSSRTTETNYICVKCBQNPVPHF 103
  |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
60 GGTHEYDNLVDSNESFDLTDCKNNGGTPASCKYNGTEGTRIRIACNNQPVHF 114
  |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

RESULT 10
NR PRH

pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
 Alternate names: RNase A
 Species: *Antilocapra americana* (pronghorn)
 Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
 Accession: A00813
 Saintema, J. J.; Gastra, W.; Munnikmsa, J.
 Mol. Evol. 13, 305-316, 1979
 Title: Primary structure of pronghorn pancreatic ribonuclease: close relation
 to the bovine enzyme
 Reference number: A00813; MUID:80075014; PMID:513141

```

;Accession: A00813
;Molecule type: protein
;Residues: 1-124 <BEI>
;Superfamily: pancreatic ribonuclease
;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
;12,41,119/Active site: His, Lys, His #status predicted
;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
;34/Binding site: carboxylate (Asn) (covalent) (partial) #status experimental

Query Match      20.3%; Score 122.5; DB 1; Length 124;
Best Local Similarity 30.3%; Pred. No. 3.3e-05;
Matches 36; Conservative 18; Mismatches 42; Indels 23; Gaps 7;

Y      4 ATFOQKHLINPI-----ICNTMDNIYIVGQCKRVNTFISSATTVKAICTGVINM 57
      | |:::| | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```
QY 1 QNWATFOQKHIIINTP-IICNTIMDNNIYVGGCKRVNTFIISATTVKAICTGV-INNV 58
Db 1 QNWAFOEKHPIINTSNINCNTIMDKSIYVGGCKERTNTFIISATTVKAICSGASTRN 60
QY 59 VLSTTRFQMLNCTRTSTTPPCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
Db 61 VLSTTRFQMLNCTRSATAPPCPNSTETNYICVKCENRLPVHFAGIGRC 111
RESULT 3
JX0085
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C:Accession: JX0085
R:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohguchi, J. Biochem. 106, 729-735, 1989
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A:Reference number: JX0085; MUID:90130374; PMID:2613682
A:Accession: JX0085
A:Molecule type: protein
A:Residues: 1-111 <NIT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10.35,104/Active site: His, Lys, His #status predicted
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted
Query Match 62.1%; Score 374; DB 2; Length 111;
Best Local Similarity 65.8%; Pred. No. 2.9e-30;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;
QY 1 QNWATFOQKHIIINTPII-CNTIMDNNIYVGGCKRVNTFIISATTVKAICTGVI-NMN 58
Db 1 QNWAKEKHIRSTSSIDCNTIMDKAIYVGGCKERTNTFIISDENVKAICSGVSPDRK 60
QY 59 VLSTTRFQMLNCTRTSTTPPCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
Db 61 ELSTTSFKLNTCIRDSITRPCCPYSPDNNKICVKCEKQLPVHFGVIGKC 111
RESULT 4
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C:Species: Rana pipiens (northern leopard frog)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C:Accession: A39035
R:Ardelt, W.; Mikulecki, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos.
A:Reference number: A39035; MUID:91093131; PMID:1985896
A:Accession: A39035
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-104 <ARD>
C:Superfamily: pancreatic ribonuclease
Query Match 45.6%; Score 274.5; DB 2; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.1e-20;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
QY 1 QNWATFOQKHIIINT-PIICNTIMDNNIYVGGCKRVNTFIISATTVKAICTGVI-NMN 58
Db 1 EDWTFQKHIIINTRDVDCNIMSTNLF----HCKDKNTIYSEPEFVKAICKGLIASKN 56
QY 59 VLSTTRFQMLNCTRTSTTPPCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
Db 57 VLITSEYFLSDC---NVTSPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 104
RESULT 5
NRWHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
```

```
N:Alternate names: RNase 1; RNase A
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A00818
R:Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A:Reference number: A00818; MUID:76277855; PMID:962870
A:Accession: A00818
A:Molecule type: protein
A:Residues: 1-124 <EMM>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,113/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
Query Match 22.5%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 1.7e-06;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;
QY 6 FQOKHII-----NTPICNTIMDNNIYVGGCKRVNTFIISATTVKAICTGVINNV 59
Db 8 FQOHMDSGNSPGNNPNYCNQMMER-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63
QY 60 L-----STTRFQMLNCTRTSTTPPCPYSSRTETNYICVKCE-NQY-PVHF 103
Db 64 LCKNGRTNCSYBSNTMHTDCROTGSSKYPNCAYKTSQKXKHIIIVACEGNYVPVHF 120
RESULT 6
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:222458
A:Accession: A35932
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BON>
A:Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C:Genetics: #status absent
C:Function:
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-145/Product: angiogenin #status predicted <MAT>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:37,64,137/Active site: His, Lys, His #status predicted
F:50-104,63-115,81-130/Disulfide bonds: #status predicted
Query Match 22.5%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 2e-06;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;
QY 33 CKRVNTFIISATTVKAIC---TGVINNV-ISTTRFQMLNCTRTSTTPPCPYSSRTE 87
Db 63 CKDVTFIHGKSNKAICGANGSPYRENLRMSKSPFQVTTCKTGSPRPPCQYRASAG 122
QY 88 TNVICKCNQYVPHF 103
Db 123 FRHWIACENGLEPVHF 138
RESULT 7
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:38:36 ; Search time 9.98129 Seconds
(without alignments)
1060.090 Million cell updates/sec

Title: US-09-961-400-15
Perfect score: 602
Sequence: 1 QNWATFOQKHINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	588.5	97.8	111	2 A27121	ribonuclease-relat
2	455	75.6	111	1 JX0120	ribonuclease-relat
3	374	62.1	111	2 JX0085	pancreatic ribonuc
4	274.5	45.6	104	2 A39035	ribonuclease-relat
5	135.5	22.5	124	1 NRWHK	pancreatic ribonuc
6	135.5	22.5	145	1 A35932	angiogenin precurs
7	133.5	22.2	167	2 S20066	pancreatic-type ri
8	132.5	22.0	124	1 NRPG	pancreatic ribonuc
9	131.5	21.8	119	2 S41111	pancreatic ribonuc
10	122.5	20.3	124	1 NRPH	pancreatic ribonuc
11	122	20.3	122	1 NRKGR	pancreatic ribonuc
12	120.5	20.0	128	1 NRCU	pancreatic ribonuc
13	120.5	20.0	149	1 NRMS	pancreatic ribonuc
14	119.5	19.9	123	1 A43825	angiogenin - pig
15	118.5	19.7	128	1 NRGPB	pancreatic ribonuc
16	117.5	19.5	128	1 NRHO	pancreatic ribonuc
17	116.5	19.4	124	1 NRCM	pancreatic ribonuc
18	116.5	19.4	124	1 NRCMM	pancreatic ribonuc
19	116.5	19.4	124	1 NRCMB	pancreatic ribonuc
20	116.5	19.4	128	1 NRKS	pancreatic ribonuc
21	114.5	19.0	124	2 S08549	ribonuclease - dom
22	114	18.9	125	1 A32474	angiogenin [valida
23	113.5	18.9	124	1 NRDEN	pancreatic ribonuc
24	113	18.8	147	1 NRHAG	angiogenin precurs
25	112.5	18.7	124	1 NRGF	pancreatic ribonuc
26	112.5	18.7	124	1 NRDEO	pancreatic ribonuc
27	112	18.6	125	1 B43825	angiogenin - rabbi
28	111.5	18.5	130	2 S22808	pancreatic ribonuc
29	110.5	18.4	124	1 NRBOB	pancreatic ribonuc

30 110.5 18.4 124 1 NRWB pancreatic ribonuc

31 110.5 18.4 124 1 NREKN pancreatic ribonuc

32 110.5 18.4 124 2 S07141 pancreatic ribonuc

33 110.5 18.4 150 1 NRBO pancreatic ribonuc

34 110.5 18.4 158 2 I61900 eosinophil-derived

35 109.5 18.2 124 1 NRSH pancreatic ribonuc

36 108.5 18.0 119 2 JX0115 pancreatic ribonuc

37 108.5 18.0 124 1 NRCS pancreatic ribonuc

38 108.5 18.0 152 1 NRRT pancreatic ribonuc

39 106.5 17.7 124 1 NRHP pancreatic ribonuc

40 106.5 17.7 125 4 A47498 seminal ribonuclea

41 106.5 17.7 150 1 NRBS seminal ribonuclea

42 104.5 17.4 124 1 NRGN pancreatic ribonuc

43 104.5 17.4 124 1 NRDEF pancreatic ribonuc

44 104 17.3 125 2 S04503 pancreatic ribonuc

45 103.5 17.2 124 2 S08546 pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
R:Accession: A27121
R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi, J. Biochem. 108, 2189-2194, 1987
A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A:Reference number: A27121; MUID:87299649; PMID:3304421
A:Accession: A27121
A:Molecule type: protein
A:Residues: 1-111 <TIT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin

Query Match 97.8%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 1.4e-51;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QNWATFOQKHINTPII-CNTIMNNIYVGGQCKRVNTFISSATTVAICTGVNNV 59
Db 1 ENWATFOQKHINTPIICNTIMNNIYVGGQCKRVNTFISSATTVAICTGVNNV 60
Qy 60 LSTTRFQNLCTRTSITPRCPYSSRTETNVCVKCENQYPVHFAGIGRCP 110
Db 61 LSTTRFQNLCTRTSITPRCPYSSRTETNVCVKCENQYPVHFAGIGRCP 111

RESULT 2

JX0120
ribonuclease-related sialic acid-binding lectin - Japanese frog
C:Species: Rana japonica (Japanese frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Accession: JX0120
R:Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi, J. Biochem. 108, 139-143, 1990
A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A:Reference number: JX0120; MUID:91035319; PMID:2229005
A:Accession: JX0120
A:Molecule type: protein
A:Residues: 1-111 <KAM>
A:Experimental source: egg
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin; pyrrolidone carboxylic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:19-72,34-82,52-97,94-111/Dsulfide bonds: #status experimental

Query Match 75.6%; Score 455; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 2.6e-38;
Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;


```
; NAME/KEY: Protein
; LOCATION: 1..104
; OTHER INFORMATION: /label= Onc
; OTHER INFORMATION: /note= "Onconase from Rana pipiens"
US-08-891-848-13

Query Match 45.6%; Score 274.5; DB 2; Length 104;
Best Local Similarity 48.6%; Pred. No. 1.7e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NNN 58
Db 1 EDWLTFOQKHINTTRDVCNDIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56

QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
Db 57 VLTTFSEFYLSDC---NVTSRPCKYKLLKSTNKFVCVTCENQAPVHFVGVGSC 104

RESULT 14
US-08-875-811-39
; Sequence 39, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-39

Query Match 45.6%; Score 274.5; DB 3; Length 105;
Best Local Similarity 48.6%; Pred. No. 1.7e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NNN 58
Db 1 EDWLTFOQKHINTTRDVCNDIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56

QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
Db 57 VLTTFSEFYLSDC---NVTSRPCKYKLLKSTNKFVCVTCENQAPVHFVGVGSC 104

RESULT 15
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-41

Query Match 45.6%; Score 274.5; DB 3; Length 355;
Best Local Similarity 48.6%; Pred. No. 7.7e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NNN 58
Db 252 EDWLTFOQKHINTTRDVCNDIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 307

QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
Db 308 VLTTFSEFYLSDC---NVTSRPCKYKLLKSTNKFVCVTCENQAPVHFVGVGSC 355

Search completed: May 7, 2004, 21:40:45
Job time : 13.7596 secs
```



```
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Embryo
US-07-921-619-1

Query Match      45.6%; Score 274.5; DB 1; Length 104;
Best Local Similarity 48.6%; Pred. No. 1.7e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVI-NMN 58
DB 1 EDWLTFOQKHINTNRDVEDCDNIMTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

QY 59 VLSITTRFOLNCTRTSITRPPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
DB 57 VLTTFSEFYLSDC---NVTSRPPCKYKLKXSTNKFVCVTCENQAPVHFVGVCSC 104
```

```
RESULT 12
US-08-467-955-1
; Sequence 1, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D. Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
```

```
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-1

Query Match      45.6%; Score 274.5; DB 1; Length 104;
Best Local Similarity 48.6%; Pred. No. 1.7e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVI-NMN 58
DB 1 EDWLTFOQKHINTNRDVEDCDNIMTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

QY 59 VLSITTRFOLNCTRTSITRPPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
DB 57 VLTTFSEFYLSDC---NVTSRPPCKYKLKXSTNKFVCVTCENQAPVHFVGVCSC 104
```

```
RESULT 13
US-08-891-848-13
; Sequence 13, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
```

APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faries, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-43

Query Match 46.1%; Score 277.5; DB 3; Length 379;
Best Local Similarity 49.5%; Pred. No. 3.7e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PLICNTIMDNVIVGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db QDWLTFQKHINTRDVDCDNIMSNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 81
QY 59 VLSTTRFOLNCTRTSITRPPCYSSRTETNYICVKCNQXVPVHPAGIGRC 109
Db 82 VLTTFSEFYLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 129

RESULT 10

US-08-283-971-1
Sequence 1, Application US/08283971
Patent No. 5529775
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D. Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
FILING DATE: 06-APR-1988
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5006 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEFAX: 718-625-0399
TELEX: No. 5529775 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1

Query Match 45.6%; Score 274.5; DB 1; Length 104;
Best Local Similarity 48.6%; Pred. No. 1.7e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PLICNTIMDNVIVGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 1 EDWLTFFQKHINTRDVDCDNIMSNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56
QY 59 VLSTTRFOLNCTRTSITRPPCYSSRTETNYICVKCNQXVPVHPAGIGRC 109
Db 57 VLTTFSEFYLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 11

US-07-921-619-1
Sequence 1, Application US/07921619
Patent No. 5595734
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D. Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,619
FILING DATE: 19920728
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5005 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEFAX: 718-625-0399
TELEX: No. 5595734 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N

APPLICANT: Wu, Yon-Neng
APPLICANT: Boix, Ester
APPLICANT: Ardelt, Wojciech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,429
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,288
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
REGISTRATION NUMBER: 38,589
REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-429-1

Query Match 46.1%; Score 277.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 7.7e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY 1 QNWATFOQKHINT-PIICNTIMDNINIVGQCKRVNTFISSATTVKAICTGVI-NNN 58
DB 1 QWLTFQKKHITRDVDCNIMTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
QY 59 VLSTTRFQNTCTRTSITPRPCYSRSTETNYICVKCENQYVHFAGIGRC 109
DB 57 VLTTFSEFYLSDC--NVTSRCKYKLLKSTNKFCTCENQAPVHFVGVGSC 104

RESULT 8
US-08-875-811-63
Sequence 63, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: Q15280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-63

Query Match 46.1%; Score 277.5; DB 3; Length 129;
Best Local Similarity 49.5%; Pred. No. 1e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY 1 QNWATFOQKHINT-PIICNTIMDNINIVGQCKRVNTFISSATTVKAICTGVI-NNN 58
DB 26 QWLTFQKKHITRDVDCNIMTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 81
QY 59 VLSTTRFQNTCTRTSITPRPCYSRSTETNYICVKCENQYVHFAGIGRC 109
DB 82 VLTTFSEFYLSDC--NVTSRCKYKLLKSTNKFCTCENQAPVHFVGVGSC 129

RESULT 9
US-08-875-811-43
Sequence 43, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:

DEVELOPMENTAL STAGE:	Oocyte
US-08-467-955-2	
Query Match	47.3%; Score 284.5; DB 1; Length 104;
Best Local Similarity	49.5%; Pred. No. 1.2e-25;
Matches	55; Conservative 16; Mismatches 31; Indels 9; Gaps 4;
QY	1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVI-NMN 58
DB	1 EDWLTFOKKHITNTRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56
QY	59 VLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCNQYVHFAGIGRC 109
DB	57 VLTTFSEFYLSDC---NVTSPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 104
RESULT 4	
US-09-394-268-1	
Sequence 1, Application US/09394268	
Patent No. 6175003	
GENERAL INFORMATION:	
APPLICANT: Saxena, Shailendra K	
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF	
FILE REFERENCE: 5013	
CURRENT APPLICATION NUMBER: US/09/394,268	
CURRENT FILING DATE: 1999-09-10	
NUMBER OF SEQ ID NOS: 8	
SOFTWARE: Patent In Ver. 2.0	
SEQ ID NO 1	
LENGTH: 104	
TYPE: PRT	
ORGANISM: Rana pipiens	
US-09-394-268-1	
Query Match	46.1%; Score 277.5; DB 3; Length 104;
Best Local Similarity	49.5%; Pred. No. 7.7e-25;
Matches	55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY	1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVI-NMN 58
DB	1 QDWLTFOKKHITNTRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56
QY	59 VLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCNQYVHFAGIGRC 109
DB	57 VLTTFSEFYLSDC---NVTSPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 104
RESULT 5	
US-09-687-748-1	
Sequence 1, Application US/09687748	
Patent No. 6423515	
GENERAL INFORMATION:	
APPLICANT: Saxena, Shailendra K	
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES	
FILE REFERENCE: 5013 US 01	
CURRENT APPLICATION NUMBER: US/09/687,748	
CURRENT FILING DATE: 2000-10-14	
PRIOR APPLICATION NUMBER: 09/394,268	
PRIOR FILING DATE: 1999-09-10	
NUMBER OF SEQ ID NOS: 8	
SOFTWARE: Patent In Ver. 2.0	
SEQ ID NO 1	
LENGTH: 104	
TYPE: PRT	
ORGANISM: Rana pipiens	
US-09-687-748-1	
Query Match	46.1%; Score 277.5; DB 4; Length 104;
Best Local Similarity	49.5%; Pred. No. 7.7e-25;
Matches	55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY	1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVI-NMN 58

```

; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; catesbeiana"
US-08-891-848-12

Query Match 97.8%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 7.4e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QNWATFOQKHIIINTPII-CNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 59
Db 1 ENWATFOQKHIIINTPII-CNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 60

Qy 60 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111

```

```

; OTHER INFORMATION: /note= "Frog Lectin from Rana
; catesbeiana"
US-08-875-811-8

Query Match 97.8%; Score 588.5; DB 3; Length 111;
Best Local Similarity 98.2%; Pred. No. 7.4e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QNWATFOQKHIIINTPII-CNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 59
Db 1 ENWATFOQKHIIINTPII-CNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 60

Qy 60 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:28:45 ; Search time 12.7596 Seconds
(without alignments)
445.066 Million cell updates/sec

Title: US-09-961-400-15

Perfect score: 602

Sequence: 1 QNWFQOKHIINTPIICNT.....ICVKCNQYPVHFAGRCGP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625371 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	97.8	111	2	US-08-891-848-12
2	588.5	97.8	111	3	US-08-875-811-8
3	284.5	47.3	104	1	US-08-467-955-2
4	277.5	46.1	104	3	US-09-394-268-1
5	277.5	46.1	104	4	US-09-687-748-1
6	277.5	46.1	104	4	US-08-626-288-1
7	277.5	46.1	104	4	US-09-095-429-1
8	277.5	46.1	129	3	US-08-875-811-63
9	277.5	46.1	379	3	US-08-875-811-43
10	274.5	45.6	104	1	US-08-283-971-1
11	274.5	45.6	104	1	US-07-921-619-1
12	274.5	45.6	104	1	US-08-467-955-1
13	274.5	45.6	104	2	US-08-891-848-13
14	274.5	45.6	105	3	US-08-875-811-39
15	274.5	45.6	355	3	US-08-875-811-41
16	274.5	45.6	358	3	US-08-875-811-51
17	272.5	45.3	104	3	US-08-875-811-1
18	272.5	45.3	104	4	US-09-394-268-2
19	272.5	45.3	104	4	US-09-071-672-1
20	272.5	45.3	104	4	US-09-687-748-2
21	272.5	45.3	104	4	US-09-966-119-1
22	272.5	45.3	106	3	US-08-875-811-28
23	272.5	45.3	107	3	US-08-875-811-30
24	272.5	45.3	112	3	US-08-875-811-32
25	272.5	45.3	251	3	US-08-875-811-59
26	272.5	45.3	254	3	US-08-875-811-61
27	272.5	45.3	355	3	US-08-875-811-49

28 272.5 45.3 355 3 US-08-875-811-57
29 272.5 45.3 355 3 US-08-875-811-64
30 272.5 45.3 366 3 US-08-875-811-55
31 269.5 44.8 104 4 US-08-626-288-2
32 269.5 44.8 104 4 US-09-095-429-2
33 267.5 44.4 105 3 US-08-875-811-24
34 267.5 44.4 105 3 US-08-875-811-26
35 263.5 43.8 358 3 US-08-875-811-45
36 263.5 43.8 365 3 US-08-875-811-53
37 249.5 41.4 107 3 US-08-875-811-20
38 239.5 39.8 111 3 US-08-875-811-22
39 236 39.2 114 3 US-09-223-118-3
40 227.5 37.8 360 3 US-08-875-811-47
41 227 37.7 114 3 US-09-223-118-2
42 226 37.5 114 3 US-09-223-118-1
43 225 37.4 114 3 US-09-223-118-4
44 206 34.2 83 3 US-08-875-811-2
45 206 34.2 83 4 US-09-071-672-3

ALIGNMENTS

RESULT 1
US-08-891-848-12
; Sequence 12 Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid

[illegible]

KW LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase;
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
 KW autoimmune disease.

XX Rana pipiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 23 /note= "Wild type Met replaced with Leu"

XX WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-PSDB; AAZ08125.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 34; Page 56; 71pp; English.

XX The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
 CC protein with Met23Leu. Carboxy terminal end of recombinant RaPLR1 has a
 CC covalently bound ligand binding moiety, which can be a LL2 antibody
 CC directed against CD22 on cancerous B cells or human chorionic
 CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases

XX Sequence 104 AA;

Query Match 46.3%; Score 278.5; DB 2; Length 104;
 Best Local Similarity 48.6%; Pred. No. 6.4e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOOKHLINT-PIICNTIMDNNTIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 58

Db 1 QDWLTFQKKHLNTRDVCNMLSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56

Qy 59 VLSTTRFQNLNCTRTSTTPRCPSYSSRTETNYICVKCENQYVHFAGIGRC 109

Db 57 VLTTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 13

AAAY28869

ID AAY28869 standard; protein; 105 AA.

XX AC AAY28869;

XX 25-JAN-2000 (first entry)

XX Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.

XX Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1;
 KW CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase;
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;

KW cancer; frog; autoimmune disease.

XX Rana pipiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"

FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"

FT Misc-difference 24

FT /note= "Wild type Met replaced with Leu"

XX WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-PSDB; AAZ08127.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 4; Page 59; 71pp; English.

XX The present sequence is a recombinant Rana pipiens ribonuclease protein
 CC (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu.
 CC Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand
 CC binding moiety, which can be a LL2 antibody directed against CD22 on
 CC cancerous B cells or human chorionic gonadotropin (hCG) effective
 CC against Kaposi's sarcoma cells. Recombinant ribonucleases can be
 CC expressed in bacteria without an N-terminal methionine due to the
 CC presence of a signal peptide that is cleaved by bacteria. The soluble
 CC expression of ribonuclease allows the proteins to be fused in-frame with
 CC ligand binding moieties to form cytotoxic fusion proteins. They can be
 CC used for treatment of cancer and autoimmune diseases

XX Sequence 105 AA;

Query Match 46.3%; Score 278.5; DB 2; Length 105;
 Best Local Similarity 48.6%; Pred. No. 6.5e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOOKHLINT-PIICNTIMDNNTIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 58

Db 2 QDWLTFQKKHLNTRDVCNMLSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 57

Qy 59 VLSTTRFQNLNCTRTSTTPRCPSYSSRTETNYICVKCENQYVHFAGIGRC 109

Db 58 VLTTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 14

AAW30301

ID AAW30301 standard; protein; 104 AA.

XX AC AAW30301;

XX 09-JUN-1998 (first entry)

XX Recombinant onc protein.

XX Onc; oncanase; ribonuclease; frog; antitumour; pancreatic cancer;
 KW human immunodeficiency virus type-1; HIV1; replication.

XX Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
 KW autoimmune disease.

XX Rana pipiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"
 FT

XX WO9950398-A2.
 PN 07-OCT-1999.
 PD 26-MAR-1999; 99WO-US006641.
 PF 27-MAR-1998; 98US-0079751P.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Rybak SM, Newton DL;
 XX WPI; 1999-610847/52.
 DR N-PSDB; AAZ08126.
 DR

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 PT

XX Claim 34; Page 57; 71pp; English.
 PS

XX The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
 CC protein with Met at position 1. Carboxy terminal end of recombinant
 CC RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2
 CC antibody directed against CD22 on cancerous B cells or human chorionic
 CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases

XX Sequence 105 AA;
 SQ

Query Match 46.8%; Score 281.5; DB 2; Length 105;
 Best Local Similarity 49.5%; Pred. No. 2.9e-24;
 Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

OY 1 QNWATFQOKHIINT-PIICNTIMDNINIVYGQCKRVNTFISSATTVAICTGVI-NMN 58
 DB 2 QDWLTFQOKHLNTRDVCNNIMSTNLP----HCKDKNTFIYSRPEPVAICKGIASKN 57

OY 59 VLSTTRFQNTCTRTSITPRPCFYSRRTETNYICVKCENQYVPHFAGIGRC 109
 DB 58 VLTTSFYLSDC---NVTSRPCKYKLKSTNTFCVTCENQAPVHFVGVC 105

RESULT 11
 AAY28879
 ID AAY28879 standard; protein; 127 AA.
 AC AAY28879;
 XX
 DT 25-JAN-2000 (first entry)
 DE Rana pipiens Clone 5a1b ribonuclease.
 DE Rana pipiens ribonuclease Clone 5a1b; RaPLR1; covalently bound; RNase;
 KW LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
 KW

KW Kaposi's Sarcoma; human chorionic gonadotropin; hCG; cancer;
 KW recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
 KW autoimmune disease.

OS Rana pipiens.
 XX

XX Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Signal_peptide
 FT /note= "Putative"
 FT Protein 24..127
 FT /label= Rana_pipiens_Clone_5a1b_ribonuclease

XX WO9950398-A2.
 PN 07-OCT-1999.
 PD 26-MAR-1999; 99WO-US006641.
 PF 27-MAR-1998; 98US-0079751P.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Rybak SM, Newton DL;
 XX WPI; 1999-610847/52.
 DR N-PSDB; AAZ08136.
 DR

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 PT

XX Disclosure; Page 69; 71pp; English.
 PS

XX The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RaPLR1).
 CC It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA
 CC library. It exhibits differences with Onconase (RTM) at amino acid
 CC residues 11, 20, 85 and 103. Carboxy terminal end of RaPLR1 has a
 CC covalently bound ligand binding moiety, which can be a LL2 antibody
 CC directed against CD22 on cancerous B cells or human chorionic
 CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases

XX Sequence 127 AA;
 SQ

Query Match 46.8%; Score 281.5; DB 2; Length 127;
 Best Local Similarity 49.5%; Pred. No. 3.7e-24;
 Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

OY 1 QNWATFQOKHIINT-PIICNTIMDNINIVYGQCKRVNTFISSATTVAICTGVI-NMN 58
 DB 24 QDWLTFQOKHLNTRDVCNNIMSTNLP----HCKDKNTFIYSRPEPVAICKGIASKN 79

OY 59 VLSTTRFQNTCTRTSITPRPCFYSRRTETNYICVKCENQYVPHFAGIGRC 109
 DB 80 VLTTSFYLSDC---NVTSRPCKYKLKSTNTFCVTCENQAPVHFVGVC 127

RESULT 12
 AAY28866
 ID AAY28866 standard; protein; 104 AA.
 AC AAY28866;
 XX
 DT 25-JAN-2000 (first entry)
 DE Recombinant RaPLR1 Met23Leu amino acid sequence.
 DE Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound;
 KW

```
CC (Rana catesbeiana) lectin used to describe the method of the invention
XX
SQ Sequence 111 AA;

Query Match 97.8%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 2.2e-59;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QNWATFOCKHINTPII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNV 59
Db 1 ENWAIFQCKHIIINPIINCNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNV 60

Qy 60 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 8
AAW06544
ID AAW06544 standard; protein; 104 AA.
XX
AC AAW06544;
XX
DI 22-AUG-1997 (first entry)
XX
DE Antitumour protein from Rana pipiens oocytes.
XX
KW Tumour; chemotherapy; radiotherapy; frog.
XX
OS Rana pipiens.
XX
PN W09639428-A1.
XX
PD 12-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US008304.
XX
PR 06-JUN-1995; 95US-00467955.
XX
PA (ALFA-) ALFACELL CORP.
XX
PI Ardelt WJ;
XX
DR WPI; 1997-043063/04.
XX
PT Antitumour proteins from Rana pipiens oocyte(s) - have fewer
PT disadvantages than chemotherapy, surgery and radiotherapy.
XX
PS Claim 8; Page 28; 45pp; English.
XX

The present sequence is a specifically claimed example of an antitumour
protein from the generic protein in AAW18224, with the molecular weight
CC 12000. This is one of two preferred proteins (the other in AAW06543) that
CC have been isolated from Rana pipiens oocytes. Both proteins have a
CC blocked amino terminal group and are essentially free of carbohydrates.
CC The proteins are used to treat tumours. Use of the peptides has fewer
CC disadvantages than chemotherapy, radiotherapy and surgery in the
CC treatment of tumours
XX
SQ Sequence 104 AA;

Query Match 47.3%; Score 284.5; DB 2; Length 104;
Best Local Similarity 49.5%; Pred. No. 1.3e-24;
Matches 55; Conservative 16; Mismatches 31; Indels 9; Gaps 4;

Qy 1 QNWATFOCKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 1 EDWLTFOCKHVTNRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

Qy 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTSEFYLSDC---NVTSRCKYKLLKSKNTFCVTCENQAPVHFVGVRG 104

RESULT 9
AAW28865
ID AAW28865 standard; protein; 104 AA.
XX
AC AAW28865;
XX
DI 25-JAN-2000 (first entry)
XX
DE Rana pipiens liver ribonuclease (RaPLR1).
XX
KW Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;
KW ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;
KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
XX
OS Rana pipiens.
XX
PN W09950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
XX
PD N-PSDB; AAZ08124.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 1; Page 55; 71pp; English.
XX

The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.
Carboxy terminal end of RaPLR1 has a covalently bound ligand binding
CC moiety, which can be a LL2 antibody directed against CD22 on cancerous B
CC cells or human chorionic gonadotrophin (hCG) effective against Kaposi's
CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
CC without an N-terminal methionine due to the presence of a signal peptide
CC that is cleaved by bacteria. The soluble expression of ribonuclease
CC allows the proteins to be fused in-frame with ligand binding moieties to
CC form cytotoxic fusion proteins. They can be used for treatment of cancer
CC and autoimmune diseases
XX
SQ Sequence 104 AA;

Query Match 46.8%; Score 281.5; DB 2; Length 104;
Best Local Similarity 49.5%; Pred. No. 2.9e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOCKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 1 QDWLTFOCKHVTNRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

Qy 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTSEFYLSDC---NVTSRCKYKLLKSKNTFCVTCENQAPVHFVGVRG 104

RESULT 10
AAW28867
ID AAW28867 standard; protein; 105 AA.
XX
AC AAW28867;
XX
DI 25-JAN-2000 (first entry)
XX
DE Recombinant Met (-1) RaPLR1.
```

```

QY 1 QNWATFOQKHIIINPILICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINMNL 60
Db 1 QNWATFOQKHIIINPILICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINMNL 60
QY 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 6
AAY28876
ID AAY28876 standard; protein; 111 AA.
XX
AC AAY28876;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant Met (-1) RaCOR1 Met22Leu Met57Leu- (His)6 protein.
XX
KW Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu- (His)6; RaCOR1;
KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW cancer; bullfrog; RNase; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
FT Misc-difference 23 /note= "Wild type Met replaced with Leu"
FT Misc-difference 58 /note= "Wild type Met replaced with Leu"
XX
XX WO9950398-A2.
XX
XX 07-OCT-1999.
XX
XX 26-MAR-1999; 99WO-US006641.
XX
XX 27-MAR-1998; 98US-0079751P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08133.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 66; 71pp; English.
XX
CC The present sequence is a recombinant Rana catesbeiana oocyte
CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6
CC tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1
CC has a covalently bound ligand binding moiety, which can be a LL2 antibody
CC directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
XX diseases
XX
SQ Sequence 111 AA;

```

```

Query Match 99.0%; Score 596; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 3e-60; Indels 0; Gaps 0;
Matches 108; Conservative 2; Mismatches 0;

QY 1 QNWATFOQKHIIINPILICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINMNL 60
Db 2 QNWATFOQKHIIINPILICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVINMNL 61

QY 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 7
AAY33321
ID AAY33321 standard; protein; 111 AA.
XX
AC AAY33321;
XX
DT 29-NOV-1999 (first entry)
XX
DE Frog lectin protein fragment.
XX
KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
KW heavy chain; cell surface marker; treatment; tumor; viral infection;
KW parasite infection; immune dysfunctional cell; autoimmune disease;
KW contraceptive; cell separation; transplantation; bone marrow ablation;
KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
XX
OS Rana catesbeiana.
XX
XX US9555073-A.
XX
PD 21-SEP-1999.
XX
PF 09-JUL-1997; 97US-00891848.
XX
PR 20-APR-1990; 90US-00510696.
PR 22-OCT-1991; 91US-0079195.
PR 04-FEB-1993; 93US-00014082.
PR 22-SEP-1993; 93US-00125462.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL, Nicholls PJ, Youle RJ;
XX
DR WPI; 1999-560488/47.
XX
PT Recombinantly fused pancreatic RNase-targeting proteins useful for
PT treating tumors, infections, immune or autoimmune disorders and as a
PT contraceptive.
XX
PS Example 3; Fig 19; 47pp; English.
XX
CC This invention describes a novel nucleic acid construct comprising
CC sequences encoding functional pancreatic RNase and a second protein
CC (preferably the light and heavy chains of an antibody) which binds a
CC specific cell surface marker on a target cell and functions as a
CC cytotoxic agent. The products can be used for selectively killing cells
CC expressing a specific surface marker. They can be used for treating
CC tumors or infected cells (e.g. cells infected by viruses (especially
CC latent or chronic virus infections, such as human immunodeficiency virus
CC (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types 1 and
CC II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster,
CC cytomegalovirus) and cells infected with parasites (such as the malaria
CC parasite)). They can also be used for treating immune dysfunctional cells
CC in immune and autoimmune diseases. Additionally, they may be used as
CC contraceptives. Finally they can also be used for cell separation in
CC vitro by selectively killing unwanted types of cells (e.g. in bone
CC marrow) prior to transplantation into a patient undergoing marrow
CC ablation by radiation or for killing leukemia cells or T-cells that would
CC cause graft-versus-host disease. This sequence represents a bullfrog
CC

```

Best Local Similarity 100.0%; Pred. No. 2.3e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 2 NWATFOQKHIIPTPIICNTIMDNNTIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 61
Db 2 NWATFOQKHIIPTPIICNTIMDNNTIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 61
QY 62 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 62 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
```

RESULT 4

AAAY28878
ID AAY28878 standard; protein; 111 AA.

XX AC AAY28878;

XX DT 25-JAN-2000 (first entry)

XX DE Recombinant Met (-1) RaCOR1 Gln1Ser amino acid sequence.

XX KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
XX KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
XX KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
XX KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
XX KW CD22; RNase; autoimmune disease.

XX OS Rana catesbeiana.
XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

XX FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"

XX FN WO9950398-A2.

XX PD 07-OCT-1999.

XX PF 26-MAR-1999; 99WO-US006641.

XX PR 27-MAR-1998; 98US-0079751P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Rybak SM, Newton DL;

XX DR WPI; 1999-610847/52.

XX DR N-PSDB; AAZ08135.

XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX PT treating cancers, viral infections or autoimmune diseases.

XX PS Claim 22; Page 68; 71pp; English.

XX CC The present sequence is a recombinant Rana catesbeiana ribonuclease
XX CC (RaCOR1) protein with Met at position 1 and Gln28Ser. Carboxy terminal end
XX CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
XX CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
XX CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
XX CC Recombinant ribonucleases can be expressed in bacteria without an N-
XX CC terminal methionine due to the presence of a signal peptide that is
XX CC cleaved by bacteria. The soluble expression of ribonuclease allows the
XX CC proteins to be fused in-frame with ligand binding moieties to form
XX CC cytotoxic fusion proteins. They can be used for treatment of cancer and
XX CC autoimmune diseases

XX SQ Sequence 111 AA;

Query Match 99.2%; Score 597; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.3e-60;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 2 NWATFOQKHIIPTPIICNTIMDNNTIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 61
Db 3 NWATFOQKHIIPTPIICNTIMDNNTIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 62
```

```
QY 62 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
```

```
Db 63 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111
```

RESULT 5

AAAY28874
ID AAY28874 standard; protein; 110 AA.

XX AC AAY28874;

XX DT 25-JAN-2000 (first entry)

XX DE Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.

XX KW Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;
XX KW RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;
XX KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
XX KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
XX KW cancer; bullfrog; RNase; autoimmune disease.

XX OS Rana catesbeiana.
XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 22 /note= "Wild type Met replaced with Leu"

XX FT Misc-difference 57 /note= "Wild type Met replaced with Leu"

XX FN WO9950398-A2.

XX PD 07-OCT-1999.

XX PF 26-MAR-1999; 99WO-US006641.

XX PR 27-MAR-1998; 98US-0079751P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Rybak SM, Newton DL;

XX DR WPI; 1999-610847/52.

XX DR N-PSDB; AAZ08132.

XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX PT treating cancers, viral infections or autoimmune diseases.

XX PS Claim 22; Page 64; 71pp; English.

XX CC The present sequence is a recombinant Rana catesbeiana oocyte
XX CC ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
XX CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety, or
XX CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
XX CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
XX CC cells. Recombinant ribonucleases can be expressed in bacteria without an
XX CC N-terminal methionine due to the presence of a signal peptide that is
XX CC cleaved by bacteria. The soluble expression of ribonuclease allows the
XX CC proteins to be fused in-frame with ligand binding moieties to form
XX CC cytotoxic fusion proteins. They can be used for treatment of cancer and
XX CC autoimmune diseases

XX SQ Sequence 110 AA;

Query Match 99.0%; Score 596; DB 2; Length 110;
Best Local Similarity 99.2%; Pred. No. 3e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

SQ Sequence 110 AA;

Query Match 100.0%; Score 602; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.1e-61;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNWATFOQKHIIINTPLICNTIMDNNIYVGGCKRVNTFISSATVKAICTGVINMNVL 60
 Db 1 QNWATFOQKHIIINTPLICNTIMDNNIYVGGCKRVNTFISSATVKAICTGVINMNVL 60
 QY 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 2

AAZ28873
 ID AAZ28873 standard; protein; 111 AA.

AC AAZ28873;
 XX

DT 25-JAN-2000 (first entry)

DE Recombinant Met (-1) RaCOR1.

KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
 KW RNase; autoimmune disease.

OS Rana catesbeiana.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

FT WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-PSDB; AAZ08131.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 63; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

SQ Sequence 111 AA;

Query Match 100.0%; Score 602; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.2e-61;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNWATFOQKHIIINTPLICNTIMDNNIYVGGCKRVNTFISSATVKAICTGVINMNVL 60
 Db 2 QNWATFOQKHIIINTPLICNTIMDNNIYVGGCKRVNTFISSATVKAICTGVINMNVL 61
 QY 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 Db 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3

AAZ28877
 ID AAZ28877 standard; protein; 110 AA.

AC AAZ28877;
 XX

DT 25-JAN-2000 (first entry)

DE Recombinant RaCOR1 Gln1Ser amino acid sequence.

KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; autoimmune disease.

OS Rana catesbeiana.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"

FT WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-PSDB; AAZ08134.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 67; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of
 CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
 CC Recombinant ribonucleases can be expressed in bacteria without an N-
 CC terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

XX Sequence 110 AA;

XX Query Match 99.2%; Score 597; DB 2; Length 110;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:25:55 ; Search time 46.9224 Seconds
(without alignments)
662.376 Million cell updates/sec

Title: US-09-961-400-15

Perfect score: 602

Sequence: 1 QNWATFQKHINTPIICNT.....ICVKCNQYPVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	602	100.0	110	2 AAY28872	Aay28872 Rana cate
2	602	100.0	111	2 AAY28873	Aay28873 Recombina
3	597	99.2	110	2 AAY28877	Aay28877 Recombina
4	597	99.2	111	2 AAY28878	Aay28878 Recombina
5	596	99.0	110	2 AAY28874	Aay28874 Recombina
6	596	99.0	111	2 AAY28876	Aay28876 Recombina
7	588.5	97.8	111	2 AAY33321	Aay33321 Frog lect
8	284.5	47.3	104	2 AAW06544	Aaw06544 Antitumou
9	281.5	46.8	104	2 AAY28865	Aay28865 Rana pipi
10	281.5	46.8	105	2 AAY28867	Aay28867 Recombina
11	281.5	46.8	127	2 AAY28879	Aay28879 Rana pipi
12	278.5	46.3	104	2 AAY28866	Aay28866 Recombina
13	278.5	46.3	105	2 AAY28869	Aay28869 Recombina
14	277.5	46.1	104	2 AAW30301	Aaw30301 Recombina
15	277.5	46.1	104	2 AAB31666	Aab31666 Amino aci
16	277.5	46.1	104	2 AAB31666	Aab31666 Northern
17	277.5	46.1	105	2 AAY32400	Aay32400 Recombina
18	277.5	46.1	379	2 AAW35126	Aaw35126 R. pipien
19	276.5	45.9	104	2 AAY28870	Aay28870 Recombina
20	276.5	45.9	105	2 AAY28871	Aay28871 Recombina
21	274.5	45.6	104	2 AAR12344	Aar12344 Protein w
22	274.5	45.6	104	2 AAR47303	Aar47303 ONCONASE
23	274.5	45.6	104	2 AAW00736	Aaw00736 Protein d
24	274.5	45.6	104	2 AAW14065	Aaw14065 Oncanase
25	274.5	45.6	104	2 AAW06543	Aaw06543 Antitumou

ALIGNMENTS

RESULT 1

AAAY28872
ID AAY28872 standard; protein; 110 AA.

XX AC AAY28872;
XX AC

DT 25-JAN-2000 (first entry)

DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.

KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
KW RNase.

XX OS Rana catesbeiana.

OS Synthetic.

PN W09950398-A2.

XX PD 07-OCT-1999.

XX PF 26-MAR-1999; 99WO-US006641.

XX PR 27-MAR-1998; 98US-0079751P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Rybak SM, Newton DJ;

XX DR WPI; 1999-610847/52.

XX DR N-FSDB; AAZ08130.

XX XX New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

XX XX Claim 22; Page 62; 71pp; English.

XX CC The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1) protein encoded by a cDNA modified for expression in E. coli. Carboxy terminal end of RaCOR1 has a covalently bound ligand binding moiety, which can be a Ll2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form

26	274.5	45.6	104	2	AAW88233	Aaw88233 Rana pipi
27	274.5	45.6	104	2	AAAY33322	Aay33322 Prog onco
28	274.5	45.6	105	2	AAW35123	Aaw35123 R. pipien
29	274.5	45.6	355	2	AAW35125	Aaw35125 R. pipien
30	274.5	45.6	358	2	AAW35130	Aaw35130 R. pipien
31	272.5	45.3	104	4	AAW31667	Aab31667 Amino aci
32	272.5	45.3	104	5	ABG31617	Abg31617 Northern
33	272.5	45.3	106	2	AAW35122	R. pipien
34	272.5	45.3	107	2	AAW35117	R. pipien
35	272.5	45.3	112	2	AAW35118	R. pipien
36	272.5	45.3	251	2	AAW35134	R. pipien
37	272.5	45.3	254	2	AAW35135	R. pipien
38	272.5	45.3	355	2	AAW35133	R. pipien
39	272.5	45.3	355	2	AAW35129	R. pipien
40	272.5	45.3	366	2	AAW35132	R. pipien
41	271.5	45.1	104	2	AAW30302	Recombina
42	267.5	44.4	104	2	AAW18224	Antitumou
43	267.5	44.4	105	2	AAW35115	R. pipien
44	267.5	44.4	105	2	AAW35116	R. pipien
45	263.5	43.8	358	2	AAW35127	R. pipien

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

[illegible]

Search completed: May 7, 2004, 21:53:05
Job time : 5.30402 secs


```

FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
FT VARIANT 64 64 L -> P.
SQ SEQUENCE 128 AA; 14406 MW; A2F4101A1A33E93B CRC64;

Query Match
Best Local Similarity 20.6%; Score 120; DB 1; Length 128;
Matches 35; Conservative 21; Mismatches 37; Indels 30; Gaps 7;

QY 2 SDMLTFQKKHL-----TNRDVCNNIM-----STNLFHCKDKNTFIYSRPEPVKAICKGI 52
DB 3 SSAMKFORQHMPEGSPSSNY-CNTMMIRNMTQGRCKPVNTFVHESLADVOAVC--- 58
QY 53 IASKNVL-----TTSEFVLSDCNVTSRP-----CKYKLLKSTNTFCVTCENQ--AP 96
DB 59 -FQKNVLCKNGQTCYQSYSRMRITDCVTSRSSFPNCSSRMSQAQKSIIVACEGDPYVP 117
QY 97 VHF 99
DB 118 VHF 120

RESULT 14
RNP PROGU STANDARD; PRT; 128 AA.
AC P04059;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Proechimys guairae (Casiragua).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Echimyidae; Proechimys.
ON NCBI_TaxID=10163;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=83000399; PubMed=7115727;
RA Beintema J.J., Krol G., Martena B.;
RT "The primary structures of pancreatic ribonucleases from African
RL porcupine and casiragua, two hystriomorph rodent species.";
CC Biochim. Biophys. Acta 705:102-110(1982).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2' 3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; A00821; NRKS.
DR HSP; P00656; 1SRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR PRINTS; P00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 128 AA; 14244 MW; 2DB58093A9D3C936 CRC64;

Query Match
Best Local Similarity 20.6%; Score 120; DB 1; Length 128;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

QY 7 FQKKHL-----TNRDVCNNIM-STNLF-HCKDKNTFIYSRPEPVKAICKGIITASKNV 58

```

```

DB 8 FQKHIDSSGSPSTNPNYCNAMKSRNMTQGRCKPVNTFVHEPLADVOAVC-----FQKNV 63
QY 59 -----LTTSEFVLSDCNVTSR-----PCYKLLKKSINTFCVTCENQ--APVHF 99
DB 64 PCXNGQSNVCYESTSNMHTDCLTSNSKFPDCLYRTSQEKSIIIVACEGPNYPVHF 120

RESULT 15
ANGI MOUSE
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N. TISSUE=Liver;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kecteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP PARTIAL SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=99192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC to actin on the surface of endothelial cells; once bound, thereby
CC angiogenin is endocytosed and translocated to the nucleus, thereby
CC promoting the endothelial invasiveness necessary for blood vessel
CC formation. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

```

```

DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 42 BY SIMILARITY.
FT ACT_SITE 41 11 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 76 N-LINKED (GLCNAC...) (30%).
SQ SEQUENCE 124 AA; 14125 MW; F57475459F697E20 CRC64;

Query Match 21.5%; Score 125; DB 1; Length 124;
Best Local Similarity 28.6%; Pred. No. 1.4e-06;
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

QY 5 LTFQKKHLTNTRDVID-----CNNTMSTNLF---HCKDKNTFYSPPEPVKAICGIIASK 56
DB 6 MKFORQHDNSGNSPNNPNYCNQMMRRKVTQGRCKPVNTFVHESLEVDKAVC-----SQK 61

QY 57 NVL-----TTFEYLSDCNVTSRP-----CKYKLKXSTNTPCVTCENQ--APVHF 99
DB 62 NVLCKNGRTNCYESNTMHTDCRQTGSSKYPNCAYKTSQKEKHLIIVACGNPVYPVHF 120

RESULT 12
ANGI_MACMU
ID ANGI_MACMU STANDARD; PRT; 146 AA.
AC Q8WN63;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin precursor (BC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG OR RNASE5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918422; PubMed=11919285;
RA Zhang J., Rosenberg H.F.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RT primate evolution."
RL Mol. Biol. Evol. 19:438-445(2002).
CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC to actin on the surface of endothelial cells; once bound,
CC angiogenin is endocytosed and translocated to the nucleus, thereby
CC promoting the endothelial invasiveness necessary for blood vessel
CC formation. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF416667; AAL61649.1; -.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; rnaaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.

```

```

DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 146 ANGIOGENIN.
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 138 138 BY SIMILARITY.
FT DISULFID 50 105 BY SIMILARITY.
FT DISULFID 63 116 BY SIMILARITY.
FT DISULFID 81 131 BY SIMILARITY.
SQ SEQUENCE 146 AA; 16301 MW; E39A89215DB2A2A4 CRC64;

Query Match 20.9%; Score 121.5; DB 1; Length 146;
Best Local Similarity 28.7%; Pred. No. 4e-06;
Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;

QY 6 TFOKKHLTNTRDVIDCNCNNIMSTNLFHCKDKNTFYSPPEPVKAIC---KGIIASKNV-LTT 61
DB 53 TMRERHLTSP-----CKDINIFVHGRRHHTAICDENGSPYGGNLRIST 97

QY 62 SEFYLSDCNVTSS---RPCKYKLKXSTNTPCVTCENQAPVH 98
DB 98 SPFOVTTCKURGGSPRPPCQYRATRGSRNIVVGCENGLPVH 138

RESULT 13
RNBP_CAVPO
ID RNBP_CAVPO STANDARD; PRT; 128 AA.
AC P00679;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RX TISSUE=Pancreas;
RX MEDLINE=77185023; PubMed=862624;
RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,
RA Beintema J.J.;
RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
RT structure and glycosylation."
RL Eur. J. Biochem. 75:91-100(1977).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3',-phosphooligonucleotides ending in C-P or U-P
CC with 2',3',-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC PIR; A00826; NRGPB.
CC HSSP; P00656; 1SRN.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; rnaaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNaseA; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.

```

RT "Solution structure of bovine angiogenin by 1H nuclear magnetic
 RL resonance spectroscopy.";
 RL Biochemistry 35:8870-8880(1996).
 CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
 CC to actin on the surface of endothelial cells; once bound,
 CC angiogenin is endocytosed and translocated to the nucleus, thereby
 CC promoting the endothelial invasiveness necessary for blood vessel
 CC formation. Angiogenin induces vascularization of normal and
 CC malignant tissues. Abolishes protein synthesis by specifically
 CC hydrolyzing cellular rRNAs. Binds tightly to placental
 CC ribonuclease inhibitor and has very low ribonuclease activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Serum and milk.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF135124; AAG47631.1; -
 CC PDB: 1AGI; 03-APR-96.
 CC PDB: 1GIO; 07-DEC-96.
 CC InterPro: IPR001427; RNaseA.
 CC Pfam: PF00074; RNaseA; 1.
 CC PRINTS: PR00794; RIBONUCLEASE.
 CC ProDom: PD000535; RNaseA; 1.
 CC SMART: SM00092; RNaseA; 1.
 CC PROSITE: PS00127; RNASE PANCREATIC; 1.
 CC Hydrolase; Nuclease; Endonuclease; Angiogenesis;
 CC Protein synthesis inhibitor; Signal; 3D-structure.
 KW
 FT SIGNAL 1 23 ANGIOGENIN-1.
 FT CHAIN 24 148
 FT ACT SITE 37 37
 FT ACT SITE 64 64
 FT ACT SITE 138 138
 FT DISULFID 50 105
 FT DISULFID 63 116
 FT DISULFID 81 131
 FT DISULFID 81 131
 SQ SEQUENCE 148 AA; 16969 MW; B7999124CBB523DD CRC64;

Query Match 22.0%; Score 128; DB 1; Length 148;
 Best Local Similarity 34.0%; Pred. No. 8.3e-07;
 Matches 33; Conservative 14; Mismatches 32; Indels 19; Gaps 5;
 QY 17 DVDQNNIMSTNLF--HCXDKNTFIYSRPEPVKAICKGLIASKN-----VLTTSEFYL 66
 DB 47 DEYCFNMKNRLTRPCCKDRNTFIHGNKNKDIKAICE---DRNGQFYRGDLRIKSEFQI 102
 QY 67 SDC---NVTSR--PKYKLLKKNSTNFCVTCENQAPVHF 99
 DB 103 TCKKHGSGSRPPCRIGATEDSRVIVGCGNGLPVHF 139
 RESULT 10
 RNP MYOCO
 ID - RNP MYOCO STANDARD; PRT; 128 AA.
 AC P00676;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASE1 OR RNS1.
 OS Myocastor coypu (Coypu) (Nutria).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Myocastoridae;
 OC Myocastor.
 OC NCBI_TaxID=10157;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Pancreas;
 RX MEDLINE=77065676; PubMed=999896;
 RA van den Berg A., van den Hende-Timmer L., Beintema J.J.;
 RT "Isolation, properties and primary structure of coypu and chinchilla
 RL pancreatic ribonuclease";
 RL Biochim. Biophys. Acta 453:400-409(1976).
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Pancreas.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR PIR: A00822; NRCU.
 DR HSP; P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNaseA; 1.
 DR PROSITE: PS00127; RNASE PANCREATIC; 1.
 KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT SITE 12 12
 FT ACT SITE 41 41
 FT ACT SITE 119 119
 FT CASBOHYD 34 34
 FT SEQUENCE 128 AA; 14267 MW; 4EB924E52B445832 CRC64;
 SQ
 Query Match 21.6%; Score 126; DB 1; Length 128;
 Best Local Similarity 29.9%; Pred. No. 1.1e-06;
 Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;
 QY 7 FQKQHL-----TNRDQVDCNNIM--STNLF--HCXDKNTFIYSRPEPVKAICKGLIASKNV 58
 DB 8 FERQHMDSRGSPSTPNYCNEMMKSRNMTQCRKPVNTFFVHEPLADVOAVC----FQKNV 63
 QY 59 L-----TTSEFVLSDCNVTSRP-----CKYKLLKKNSTNFCVTCENQ--APVHF 99
 DB 64 LCKNGQTCYQSNMNHITDCRVTSNSDYPNCSYRTSQEKSIVVACBGNFVPVHF 120
 RESULT 11
 RNP BALAC
 ID - RNP BALAC STANDARD; PRT; 124 AA.
 AC P00673;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASE1 OR RNS1.
 OS Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaenopteridae; Balaenoptera.
 OC NCBI_TaxID=9767;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76277855; PubMed=962870;
 RA Emmens M., Welling G.W., Beintema J.J.;
 RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
 RL ribonuclease";
 RL Biochem. J. 157:317-323(1976).
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Pancreas.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR PIR: A00818; NRWHK.
 DR HSP; P00656; ISRN.

FT ACT_SITE 37 37 BY SIMILARITY.
 FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 137 137 BY SIMILARITY.
 FT DISULFID 50 104 BY SIMILARITY.
 FT DISULFID 63 115 BY SIMILARITY.
 FT DISULFID 81 130 BY SIMILARITY.
 SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4D CRC64;
 Query Match 22.4%; Score 130.5; DB 1; Length 145;
 Best Local Similarity 38.2%; Pred. No. 4.4e-07;
 Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;
 QY 31 CKDKNFTFYSPPEVKAIC--KGIIASKNV-LTTSEFYLSDCNVTSR-----PCKYKLKKS 83
 DB 63 CKDNTFTHTKNNIKAIKGGKSPYGNLRISKSRFQVTTCTHKGRSPRPVYRASKG 122
 QY 84 TNTFCVTCENQAPVHF 99
 DB 123 FRYIIIGCENGWVPHF 138

RESULT 8

ANGI_CERAE
 ID_ANGI_CERAE STANDARD; PRT; 146 AA.
 AC O8WN66;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.1.27.-) (Ribonuclease 5) (RNase 5).
 GN ANG OR RNASES.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21918422; PubMed=11919285;
 RA Zhang J., Rosenberg H.P.;
 RT "Diversifying selection of the tumor-growth promoter angiogenin in
 RT primate evolution.";
 RL Mol. Biol. Evol. 19:439-445(2002).
 CC -1- FUNCTION: May function as a tRNA-specific ribonuclease that binds
 CC to actin on the surface of endothelial cells; once bound,
 CC angiogenin is endocytosed and translocated to the nucleus, thereby
 CC promoting the endothelial invasiveness necessary for blood vessel
 CC formation. Angiogenin induces vascularization of normal and
 CC malignant tissues. Abolishes protein synthesis by specifically
 CC hydrolyzing cellular tRNAs (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF441664; AAL61646.1;
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnasea; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00127; RNASE_PANCREATIC; 1.
 DR HydroLase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 24
 FT CHAIN 25 146 ANGIOGENIN.
 FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
 FT SIMILARITY).

FT ACT_SITE 37 37 BY SIMILARITY.
 FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 138 138 BY SIMILARITY.
 FT DISULFID 50 105 BY SIMILARITY.
 FT DISULFID 63 116 BY SIMILARITY.
 FT DISULFID 81 131 BY SIMILARITY.
 SQ SEQUENCE 146 AA; 16444 MW; 27860112E85B8DF9 CRC64;
 Query Match 22.4%; Score 130.5; DB 1; Length 146;
 Best Local Similarity 30.7%; Pred. No. 4.4e-07;
 Matches 31; Conservative 17; Mismatches 30; Indels 23; Gaps 4;
 QY 6 TFOKKHLNTRDVCNIMSTNLPHCKDKNFIFYSRPFVKAIC---KGIIASKNV-LTT 61
 DB 53 TMRKHLTSP-----CKDINTFIHGRHHIKAICDGENGPNFYGENLRISK 97
 QY 62 SEFYLSDCNVTSS---RPCKYKLKKSNTFCVTCENQAPVH 98
 DB 98 SPFQVTTCNLRGSGSPRPFCQYRATRGSRNIVVGCENGLPVH 138
 RESULT 9
 ANGI_BOVIN
 ID_ANGI_BOVIN STANDARD; PRT; 148 AA.
 AC P10152; O9GKP9;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Angiogenin-1 precursor (EC 3.1.27.-).
 GN ANGI OR ANG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Liver;
 RA Chang S.-I.;
 RT "Cloning, sequencing, and expression of bovine angiogenin.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC [2]
 CC SEQUENCE OF 24-148.
 CC TISSUE=Milk;
 CC MEDLINE=89065101; PubMed=3197838;
 CC Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.;
 CC "The complete amino acid sequence of bovine milk angiogenin.";
 CC FEBS Lett. 241:41-45(1988).
 CC [3]
 CC SEQUENCE OF 24-148.
 CC TISSUE=Plasma;
 CC MEDLINE=89375344; PubMed=2775757;
 CC Bond M.D., Strydom D.J.;
 CC "Amino acid sequence of bovine angiogenin.";
 CC Biochemistry 28:6110-6113(1989).
 CC [4]
 CC CHARACTERIZATION, AND SEQUENCE OF 25-55.
 CC TISSUE=Plasma;
 CC MEDLINE=89118214; PubMed=3064806;
 CC Bond M.D., Vallee B.L.;
 CC "Isolation of bovine angiogenin using a placental ribonuclease
 CC inhibitor binding assay";
 CC Biochemistry 27:6282-6287(1988).
 CC [5]
 CC X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 CC MEDLINE=95224057; PubMed=7708754;
 CC Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;
 CC "Crystal structure of bovine angiogenin at 1.5-A resolution.";
 CC Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
 CC [6]
 CC STRUCTURE BY NMR.
 CC MEDLINE=96280645; PubMed=8688423;
 CC Lequin O., Albarret C., Bontems F., Spik G., Lallemand J.-Y.;


```

QY 3 DWLTFQKKHLNTRDVCNNIMSTNLF-----HCKDKNTFIYSRPEPVKAICKGIASKNV 58
Db 24 NWATFOQKHINTPIINCNTNMNNIYVGGCKEVNTFISSATTVKAICTGVI-NMNV 82
QY 59 LTTSEFYLSDC---NVTSRPKYKLLKSTNFCVTCENQAPVHFVGVGHC 105
Db 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNIVKRCENQYPVHFAGIGRC 132

RESULT 3
LECS_RANJA
ID _LECS_RANJA STANDARD; PRT; 111 AA.
AC P18839;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sialic acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese redbell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Titani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs."
RL J. Biochem. 108:139-143(1990).
CC -!- FUNCTION: The S-lectins in frog eggs may be involved in the
CC fertilization and development of the frog embryo. This lectin
CC preferentially agglutinate a large variety of tumor cells, but it
CC does not agglutinate non-transformed cells and erythrocytes.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR HSSP; P11916; IBC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Pyridoxal carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT DISULFID 34 82 BY SIMILARITY.
FT DISULFID 52 97 BY SIMILARITY.
FT DISULFID 94 111 PROBABLE.
SQ SEQUENCE 111 AA; 12326 MW; FDEBDF3834ED679 CRC64;

Query Match 48.2%; Score 280.5; DB 1; Length 111;
Best Local Similarity 44.5%; Pred. No. 3.1e-23;
Matches 49; Conservative 19; Mismatches 35; Indels 7; Gaps 2;

QY 3 DWLTFQKKHLNTRDVCNNIMSTNLF-----HCKDKNTFIYSRPEPVKAICKGIASKNV 58
Db 2 NWAKFOEKHPNPTSNINCNTIMDKSIYVGGCKERTNFISSATTVKAICSGASTNRV 61
QY 59 LTTSEFYLSDC---NVTSRPKYKLLKSTNFCVTCENQAPVHFVGVGHC 105
Db 62 LSTTRFQNTCTRTSITPRPCPYSSRTETNIVKRCENRNPVHFAGIGRC 111

RESULT 4
RNPL_RANCA
ID _RNPL_RANCA STANDARD; PRT; 111 AA.
AC P14626;

```

```

DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, liver (EC 3.1.27.5).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90130374; PubMed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT liver."
RL J. Biochem. 106:729-735(1989).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR HSSP; P11916; IBC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Pyridoxal carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT DISULFID 34 82 BY SIMILARITY.
FT DISULFID 52 97 BY SIMILARITY.
FT DISULFID 94 111 PROBABLE.
SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 45.4%; Score 264.5; DB 1; Length 111;
Best Local Similarity 42.7%; Pred. No. 1.6e-21;
Matches 47; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

QY 3 DWLTFQKKHLNTRDVCNNIMSTNLF-----HCKDKNTFIYSRPEPVKAICKGIASKNV 58
Db 2 NWAKFOEKHIRSTSIDCNTIMDKAIYVGGCKERTNFISSDNVKAICSGVSPORKE 61
QY 59 LTTSEFYLSDC---NVTSRPKYKLLKSTNFCVTCENQAPVHFVGVGHC 105
Db 62 LSTTRFQNTCTRTSITPRPCPYSSRTETNIVKRCENRNPVHFAGIGRC 111

RESULT 5
RNP_IGUIG
ID _RNP_IGUIG STANDARD; PRT; 119 AA.
AC P80287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS Iguana iguana (Common iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=8517;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT ribonuclease."
RL Eur. J. Biochem. 219:641-646(1994).

```



```

FT DISULFID 48 90
FT DISULFID 87 104
FT HELIX 3 10
FT STRAND 11 12
FT STRAND 19 22
FT STRAND 23 24
FT TURN 26 30
FT TURN 33 38
FT STRAND 33 38
FT HELIX 41 45
FT HELIX 46 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 94.7%; Score 551; DB 1; Length 104;
Best Local Similarity 96.1%; Pred. No. 3.9e-52;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 62
DB 2 DDLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
QY 63 EFLYSDCNVTRSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
DB 62 EFLYSDCNVTRSPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 2
ID RNPO RANCA STANDARD; PRT; 133 AA.
AC P11916; Q9PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-
DE binding lectin) (SBL-C).
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity."
RL J. Biol. Chem. 273:6395-6401(1998).
RN [2]
RP SEQUENCE OF 23-133.
RC TISSUE=Egg;
RX MEDLINE=87299649; PubMed=3304421;
RX Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana
RT catesbeiana) eggs."
RL Biochemistry 26:2189-2194(1987).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.
RX MEDLINE=92220613; PubMed=1373237;
RX Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes."
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [4]

```

```

RP RP
RC RC
RX RX
RA RA
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana
RT catesbeiana eggs."
RL Glycobiology 3:37-45(1993).
RN RN
RP STRUCTURE BY NMR OF 23-133.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog)."
RL J. Mol. Biol. 283:231-244(1998).
CC CC
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine
CC residues with a 3' flanking guanine. Hydrolyzes poly(U) and poly(C)
CC as substrates, and prefers the former. The S-lectins in frog eggs
CC may be involved in the fertilization and development of the frog
CC embryo. This lectin agglutinates various animal cells, including
CC normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC human origin. It is cytotoxic against several tumor cells.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF039104; AAD10702.1; -.
DR FIR; A27121; A27121.
DR PDB; 1BC4; 28-OCT-98.
DR PDB; 1M07; 21-JAN-93.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 22
FT CHAIN 23 133 RIBONUCLEASE, OOCYTES.
FT MOD RES 23 23 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 32 32
FT ACT_SITE 57 57
FT ACT_SITE 125 125
FT ACT_SITE 41 93
FT DISULFID 41 93
FT DISULFID 56 103
FT DISULFID 74 118
FT DISULFID 115 132
FT HELIX 25 32
FT HELIX 41 45
FT TURN 48 49
FT STRAND 59 63
FT HELIX 67 73
FT TURN 74 74
FT STRAND 79 84
FT STRAND 90 95
FT STRAND 105 110
FT STRAND 114 119
FT TURN 120 121
FT STRAND 122 129
SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 49.3%; Score 287; DB 1; Length 133;
Best Local Similarity 49.1%; Pred. No. 7.8e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.30402 Seconds
(without alignments)
1030.796 Million cell updates/sec

Title: US-09-961-400-13
Perfect score: 582
Sequence: 1 MSDWLTFQKKLHTRDVDC.....TFCVTCENQAPVHFVGWGHG 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	94.7	104	1	RN30_RANPI
2	287	49.3	133	1	RNPO_RANCA
3	280.5	48.2	111	1	LECS_RANJA
4	264.5	45.4	111	1	RNPL_RANCA
5	144	24.7	119	1	RNP_IGUIG
6	132	22.7	124	1	RNP_GALMU
7	130.5	22.4	145	1	ANGR_MOUSE
8	130.5	22.4	146	1	ANGI_CERAE
9	128	22.0	148	1	ANGI_BOVIN
10	126	21.6	128	1	RNP_MYOCC
11	125	21.5	124	1	RNP_BALAC
12	121.5	20.9	126	1	ANGI_MACMU
13	120	20.6	128	1	RNPB_CAVPO
14	120	20.6	128	1	RNP_PROGU
15	119.5	20.5	145	1	ANGI_MOUSE
16	118.5	20.4	146	1	ANGI_PAPHA
17	118	20.3	124	1	RNP_CHIBR
18	117	20.1	128	1	RNP_HYDHY
19	116	19.9	125	1	ANGI_RABIT
20	115	19.8	146	1	ANGI_MIOIA
21	114	19.6	124	1	RNP_HIPAM
22	113.5	19.5	147	1	RNS4_PANTR
23	113	19.4	147	1	ANGI_HUMAN
24	113	19.4	147	1	ANGI_PANTR
25	113	19.4	156	1	ECF3_MOUSE
26	112	19.2	124	1	RNP_FIG
27	112	19.2	128	1	RNP_HYSCR
28	112	19.2	150	1	RNP_BOVIN
29	112	19.2	156	1	RNP_MYOGL
30	111.5	19.2	147	1	RNS4_HUMAN
31	111	19.1	128	1	RNP_HORSE
32	111	19.1	146	1	ANGI_SALSC
33	111	19.1	167	1	RNBR_BOVIN

34 110.5 19.0 123 1 ANGI_PIG
35 110.5 19.0 155 1 ECF1_MOUSE
36 110 18.9 124 1 RNPA_CAVPO
37 110 18.9 141 1 RNBR_GIRCA
38 110 18.9 146 1 ANGI_SAGOE
39 110 18.9 151 1 RNBR_AXIPR
40 110 18.9 156 1 ECP2_MOUSE
41 109 18.7 123 1 ANG2_BOVIN
42 109 18.7 124 1 RNP_AEPME
43 109 18.7 124 1 RNP_SHEEP
44 109 18.7 124 1 RNP_SHEEP
45 108.5 18.6 150 1 RNS6_SAISC

ALIGNMENTS

RESULT 1
RN30_RANPI
ID RN30_RANPI STANDARD; PRT; 104 AA.
AC P22069;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P-30 protein (EC 3.1.27.-) (Onconase).
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=91093131; PubMed=985896;
RA Ardelit W., Mikulski S.M., Shogen K.;
RT "Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";
RL J. Biol. Chem. 266:245-251(1991).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=93066156; PubMed=1438177;
RA Mosimann S.C., Johns K.L., Ardelit W., Mikulski S.M., Shogen K., James M.N.G.;
RT "Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";
RL Proteins 14:392-400(1992).
RN [3]
RX X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
MEDLINE=94166079; PubMed=8120892;
RA Mosimann S.C., Ardelit W., James M.N.G.;
RT "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";
RL J. Mol. Biol. 236:1141-1153(1994).
CC -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vivo. It exhibits a ribonuclease-like activity against high molecular weight ribosomal RNA.
CC -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PDB; IONC; 31-JAN-94.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF000074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW Pyridolone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT ACT_SITE 10 10
FT ACT_SITE 31 31
FT ACT_SITE 97 97
FT DISULFID 19 68
FT DISULFID 30 75

Search completed: May 7, 2004, 21:54:54
Job time : 9.5276 secs


```
Query Match      20.6%; Score 120; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 5.3e-05;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

QY 7 FQKHL-----TNRDVCNNIM--STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
Db 8 FQCHIDSSGSPSTFNPCNMMKSRNMTQERCKPNTFVHEPLADVQAVC-----FQKNV 63

QY 59 -----LTTSEFYLSDCNVTSR-----PCKYKLKSKTNTFCVTCENQ--APVHF 99
Db 64 PCKNGQSNVCYSTSNMHTDCLRTSNKPPDCLYRTSQEKSIIIVACEGPNVPVHF 120

RESULT 11
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N:Alternate names: RNase IB
C:Species: Cavia porcellus (guinea pig)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A00826
R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gastra, W.; Beintema, J.J.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A:Reference number: A91247; MUID:77185023; PMID:862624
A:Accession: A00826
A:Molecule type: protein
A:Residues: 1-128 <VAN>
A>Note: 64-Pro was also found
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12.41.119/Active site: His, Lys, His #status predicted
F:21.34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted

Query Match      20.6%; Score 120; DB 1; Length 128;
Best Local Similarity 28.5%; Pred. No. 5.3e-05;
Matches 35; Conservative 21; Mismatches 37; Indels 30; Gaps 7;

QY 2 SDLWTFQKHL-----TNRDVCNNIM--STNLFHCKDKNTFIYSRPEPVKAICKGI 52
Db 3 SSAMKFORQHMDSGSPSTNANYCNMIRNMTQGRCKPNTFVHEPLADVQAVC--- 58

QY 53 IASKNVL-----TTSEFYLSDCNVTSR-----CKYKLKSKTNTFCVTCENQ--AP 96
Db 59 -FQKNVCKNGQTCYQSYRMRITDCRTVTSSTSSKFPNCSYRMSQAKSIIVACEGDPVVP 117
QY 97 VHF 99
Db 118 VHF 120

RESULT 12
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:2222458
A:Accession: A35932
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BON>
A:Cross-references: GB:U22516; NID:G726325; PIDN:AAA91366.1; PID:G726326
C:Genetics:
A:Introns: #status absent
A:Function:
A>Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease
```

```
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-145/Product: angiogenin #status predicted <MAT>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:37.64.137/Active site: His, Lys, His #status predicted
F:50-104, 63-115, 81-130/Disulfide bonds: #status predicted

Query Match      20.5%; Score 119.5; DB 1; Length 145;
Best Local Similarity 30.8%; Pred. No. 6.8e-05;
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;

QY 10 KHLNTRDVC-----CNNIMSTNLF--HCKDKNTFIYSRPEPVKAIC--KGIASKN 57
Db 32 KFLTQHDDAKPKGRDDRYCERMMKRSRLTSFCKDNTFIHGKSNKAIKCAIGANGSPYREN 91

QY 58 V-LTTSEFYLSDCNVTSS-----RPCKYKLKSKTNTFCVTCENQAPVHF 99
Db 92 LRMSKSPFQVTTCKHTGSGPRPPCQYRASAGFRHVVIIACENGLPVHF 138

RESULT 13
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) - Chinchilla brevicaudata (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00820
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A:Reference number: A90612; MUID:77065676; PMID:999896
A:Accession: A00820
A:Molecule type: protein
A:Residues: 1-124 <VAN>
A>Note: a second component of chinchilla ribonuclease has 32-Asp
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12.41.119/Active site: His, Lys, His #status predicted
F:26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match      20.3%; Score 118; DB 1; Length 124;
Best Local Similarity 27.0%; Pred. No. 8.2e-05;
Matches 33; Conservative 19; Mismatches 42; Indels 28; Gaps 6;

QY 2 SDLWTFQKHL-----TNRDVCNNIM--STNLFHCKDKNTFIYSRPEPVKAICKGII 53
Db 3 SSAMKFORQHMDSGSPSTNANYCNMIRNMTQGRCKPNTFVHEPLADVQAVC--- 58

QY 54 ASKNV-----LTTSEFYLSDCNVTSRP-----CKYKLKSKTNTFCVTCENQ--APV 97
Db 59 FQKNVCKNGQSNVCYQSNMHTDCLRTSNKFPNCSYRMSQAKSIIVACEGPNVPV 118
QY 98 HF 99
Db 119 HF 120

RESULT 14
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) - capybara
N:Alternate names: RNase 1; RNase A
C:Species: Hydrochaeris hydrochaeris (capybara, carpincho)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 29-Oct-1999
C:Accession: A00824
R:Beintema, J.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amir
A:Reference number: A92957; MUID:87036770; PMID:6571219
A:Accession: A00824
A:Molecule type: protein
A:Residues: 1-128 <BEI>
C:Superfamily: pancreatic ribonuclease
```

R;Bond, M.D.; Strydom, D.J.
Biochemistry 28, 6110-6113, 1989
A;Title: Amino acid sequence of bovine angiogenin.
A;Reference number: A32474; MUID:89375344; PMID:2775757
A;Accession: A32474
A;Molecule type: protein
A;Residues: 1-125 <BON>
A;Experimental source: plasma
R;Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.
FEBS Lett. 241, 41-45, 1988
A;Title: The complete amino acid sequence of bovine milk angiogenin.
A;Reference number: S02001; MUID:89065101; PMID:3197838
A;Accession: S02001
A;Molecule type: protein
A;Residues: 1-125 <MAE>
A;Experimental source: milk
R;Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
submitted to the Brookhaven Protein Data Bank, January 1995
A;Reference number: A65065; PDB:1AG1
A;Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125
R;Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
A;Title: Crystal structure of bovine angiogenin at 1.5 Angstroms resolution.
A;Reference number: A58315; MUID:95224057; PMID:7708754
A;Contents: annotation; X-ray crystallography, 1.5 angstroms
R;Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
submitted to the Brookhaven Protein Data Bank, April 1996
A;Reference number: A65709; PDB:1GTO
A;Contents: annotation; Conformation by (1)H-NMR, residues 1-125
R;Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
Biochemistry 35, 8870-8880, 1996
A;Title: Solution structure of bovine angiogenin by (1)H nuclear magnetic resonance spectroscopy.
A;Reference number: A58821; MUID:96280645; PMID:8688423
A;Contents: annotation; Conformation by (1)H-NMR
R;Reisdorf, C.; Abergei, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.
Eur. J. Biochem. 224, 811-822, 1994
A;Title: Proton resonance assignments and secondary structure of bovine angiogenin.
A;Reference number: S48212; MUID:95010071; PMID:7925406
A;Contents: annotation; Conformation by (1)H-NMR
C;Function:
A;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C;Superfamily: pancreatic ribonuclease
C;Keywords: angiogenesis; hydrolase; nucleic acid degradation
F;60-68/Region: receptor binding #status predicted
F;14, 41, 115/Active site: His, Lys, His #status predicted
F;27-82, 40-93, 58-108/Disulfide bonds: #status experimental
Query Match 22.0%; Score 128; DB 1; Length 125;
Best Local Similarity 34.0%; Pred. No. 8.2e-06;
Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;
QY 17 DVDCCNNSTNLF--HCKDKNTFIYSRPPVKAICKGIIASKN-----VLTSRPHYL 66
Db 24 DEYCFNMKNRLRTPCKDRNTFHGNKNDKAICE-----DRNGQYRGDLRIKSEFQI 79
QY 67 SDG---NVTSR-PCKYKLKSTNTFCVTCENQAPVHF 99
Db 80 TICKHGSSPPCKRYGATESRVIVGCCGLPVHF 116
RESULT 8
NRCU
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00822
A;Molecule type: protein

A;Residues: 1-128 <VAN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12, 41, 119/Active site: His, Lys, His #status predicted
F;26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 21.6%; Score 126; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 1.3e-05;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;
QY 7 FQKXHL-----TNRDVCNNIM-STNLF--HCKDKNTFIYSRPPVKAICKGIIASKNV 58
Db 8 FERQHMDSRGSPTNPYCNEMKSRNMTQGRCKPNTFVHEPLADVAVC-----FQKNV 63
QY 59 L-----TTSEFYLSDCNVTSRP-----CKYKLKSTNTFCVTCRNQ--APVHF 99
Db 64 LCKNGQTCYQSGNSNMHITDCRVTSNSDYPNCSYRTSQEKSIVVACENPVVPVHF 120
RESULT 9
NRWK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A00818
R;Jennens, M.; Wellington, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease
A;Reference number: A00818; MUID:76277855; PMID:962870
A;Accession: A00818
A;Molecule type: protein
A;Residues: 1-124 <EMW>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12, 41, 119/Active site: His, Lys, His #status predicted
F;26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 21.5%; Score 125; DB 1; Length 124;
Best Local Similarity 28.6%; Pred. No. 1.6e-05;
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;
QY 5 LTFQKKHLNTRDVD-----CNNIMSTNLF--HCKDKNTFIYSRPPVKAICKGIIASK 56
Db 6 MKFORQHMDSGNSFGNNPNYCNQMMRKMKTQGRCKPNTFVHESLEDVKAVC-----SQK 61
QY 57 NVL-----TTSEFYLSDCNVTSRP-----CKYKLKSTNTFCVTCENQ--APVHF 99
Db 62 NVLCNKGNTCYESNSTWHITDCRQTGSSKYPNCAYKTSQKEKHIIIVACGNPVVPVHF 120
RESULT 10
NRKS
pancreatic ribonuclease (EC 3.1.27.5) - casiragua
C;Species: Proechimys guairae (casiragua)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 30-Sep-1993
C;Accession: A00821
R;Beintema, J.J.; Knol, G.; Martena, B.
Biochim. Biophys. Acta 705, 102-110, 1982
A;Title: The primary structures of pancreatic ribonucleases from African porcupine and
A;Reference number: A90644; MUID:83000399; PMID:7115727
A;Accession: A00821
A;Molecule type: protein
A;Residues: 1-128 <BRI>
A;Note: residues 67-78 were positioned primarily by homology with other ribonucleases
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12, 41, 119/Active site: His, Lys, His #status predicted
F;26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:38:36 ; Search time 9 5276 Seconds
(without alignments)
1060.090 Million cell updates/sec

Title: US-09-961-400-13
Perfect score: 582
Sequence: 1 MSDWLTQKKHLNTRDVC.....TFCVTCENQAPVHFGVGHC 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28366 segs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_78:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	551	94.7	104	2	A39035	ribonuclease-relat
2	287	49.3	111	2	A27121	ribonuclease-relat
3	280.5	48.2	111	1	JX0120	ribonuclease-relat
4	264.5	45.4	111	2	JX0085	pancreatic ribonuc
5	144	24.7	119	2	S41111	pancreatic ribonuc
6	132	22.7	124	1	NRUI	pancreatic ribonuc
7	128	22.0	125	1	A32474	angiogenin [valida
8	126	21.6	128	1	NRUC	pancreatic ribonuc
9	125	21.5	124	1	NRWHK	pancreatic ribonuc
10	120	20.6	128	1	NRKS	pancreatic ribonuc
11	120	20.6	128	1	NRGPB	pancreatic ribonuc
12	119.5	20.5	145	1	A35932	angiogenin precurs
13	118	20.3	124	1	NRCE	pancreatic ribonuc
14	117	20.1	128	1	NRVY	pancreatic ribonuc
15	116	19.9	125	1	B43825	pancreatic ribonuc
16	114	19.6	124	1	NRHP	angiogenin - rabbi
17	113	19.4	147	1	NRHUG	pancreatic ribonuc
18	112	19.2	124	1	NRBOB	pancreatic ribonuc
19	112	19.2	124	1	NRPG	pancreatic ribonuc
20	112	19.2	128	1	NRPO	pancreatic ribonuc
21	112	19.2	150	1	NRBO	pancreatic ribonuc
22	111.5	19.2	147	2	I52489	ribonuclease 4 (EC
23	111	19.1	124	2	S08549	ribonuclease - dom
24	111	19.1	128	1	NRHO	pancreatic ribonuc
25	111	19.1	167	2	S20066	pancreatic-type ri
26	110.5	19.0	123	1	A43825	angiogenin - pig
27	110.5	19.0	155	2	JC6159	eosinophil-associ
28	110	18.9	124	1	NRGPA	pancreatic ribonuc
29	110	18.9	156	2	JC6160	eosinophil-associ

30	109	18.7	124	1	NBSH	pancreatic ribonuc
31	109	18.7	124	1	NRPRH	pancreatic ribonuc
32	109	18.7	124	2	S07141	pancreatic ribonuc
33	108	18.6	124	1	NRWB	pancreatic ribonuc
34	108	18.6	124	1	NRGN	pancreatic ribonuc
35	107	18.4	124	1	NRGF	pancreatic ribonuc
36	105	18.0	124	1	NRDEO	pancreatic ribonuc
37	105	18.0	124	1	NRDM	pancreatic ribonuc
38	105	18.0	124	1	NRMM	pancreatic ribonuc
39	105	18.0	124	1	NRMB	pancreatic ribonuc
40	105	18.0	128	1	NRW2	pancreatic ribonuc
41	104	17.9	124	1	NRHY	pancreatic ribonuc
42	103	17.7	124	1	NRDER	pancreatic ribonuc
43	103	17.7	124	1	NRDEN	pancreatic ribonuc
44	103	17.7	124	1	NRKN	pancreatic ribonuc
45	102	17.5	124	1	NRDEF	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C:Species: Rana pipiens (northern leopard frog)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C:Accession: A39035

R:Ardelet, W.; Mikulski, S.M.; Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and ear

A:Reference number: A39035; MUID:91093131; PMID:1985896

A:Accession: A39035

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <ARD>

C:Superfamily: pancreatic ribonuclease

Query Match 94.7%; Score 551; DB 2; Length 104;
Best Local Similarity 96.1%; Pred. No. 2.5e-48;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY	3	DWLTFQKKHLNTRDVCNINMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLITS	62
Db	2	DWLTFQKKHLNTRDVCNINMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLITS	61
QY	63	EFYLSDCNVTSRPCYKLLKSTNTFCVTCENQAPVHFGVGHC	105
Db	62	EFYLSDCNVTSRPCYKLLKSTNTFCVTCENQAPVHFGVGSC	104

RESULT 2

A27121

ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C:Accession: A27121

R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanag

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <TIT>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match 49.3%; Score 287; DB 2; Length 111;
Best Local Similarity 49.1%; Pred. No. 8.1e-22;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY	3	DWLTFQKKHLNTRDVCNINMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKNV	58
Db	2	NWATFQKKHLNTRDVCNINMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKNV	60

Qy	1	MSDWLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT	60
Db	1	MODWLTTFQKKHLTNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT	60
Qy	61	TSEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC	105
Db	61	TFEYLSDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGVGHC	105

Search completed: May 7, 2004, 21:51:57
Job time : 33.6904 secs

```
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
; FEATURE:
; OTHER INFORMATION: ribonuclease (RaPLR1)
US-09-948-391A-2

Query Match          96.9%; Score 564; DB 10; Length 104;
Best Local Similarity 99.0%; Pred. No. 4.4e-57;
Matches 102; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DDLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 62
Db 2 DDLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 61
Qy 63 EFYLSDCNVTSRPCKYKIKKSTNTFCVTCENQAPVHFVGVGHC 105
Db 62 EFYLSDCNVTSRPCKYKIKKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 13
US-09-948-391A-4
; Sequence 4, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met23Leu substitution
; OTHER INFORMATION: (recombinant RaPLR1 Met23Leu)
US-09-948-391A-4

Query Match          96.9%; Score 564; DB 10; Length 104;
Best Local Similarity 98.1%; Pred. No. 4.4e-57;
Matches 101; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DDLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 62
Db 2 DDLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTF 61
Qy 63 EFYLSDCNVTSRPCKYKIKKSTNTFCVTCENQAPVHFVGVGHC 105
Db 62 EFYLSDCNVTSRPCKYKIKKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 14
US-09-961-400-4
```

```
; Sequence 4, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-4
```

```
Query Match          96.9%; Score 564; DB 10; Length 104;
Best Local Similarity 98.1%; Pred. No. 4.4e-57;
Matches 101; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DDLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 62
Db 2 DDLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTF 61
Qy 63 EFYLSDCNVTSRPCKYKIKKSTNTFCVTCENQAPVHFVGVGHC 105
Db 62 EFYLSDCNVTSRPCKYKIKKSTNTFCVTCENQAPVHFVGVGHC 104
```

```
RESULT 15
US-09-948-391A-8
; Sequence 8, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 and Met24Leu
; OTHER INFORMATION: substitution (recombinant Met(-1) RaPLR1 Met23Leu)
US-09-948-391A-8
```

```
Query Match          96.2%; Score 560; DB 10; Length 105;
Best Local Similarity 96.2%; Pred. No. 1.3e-56;
Matches 101; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```



```
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with GlnIser substitution
; OTHER INFORMATION: (recombinant RaPIRI Q1S)
US-09-948-391A-11

Query Match          99.1%; Score 577; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SDWLTFOKKHLTNTTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 61
Db 1 SDWLTFOKKHLTNTTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60

Qy 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 6
US-09-961-400-11
; Sequence 11, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-11

Query Match          99.1%; Score 577; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SDWLTFOKKHLTNTTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 61
Db 1 SDWLTFOKKHLTNTTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60

Qy 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 7
US-09-961-400-9
```

```
; Sequence 9, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-9

Query Match          98.8%; Score 575; DB 10; Length 111;
Best Local Similarity 98.1%; Pred. No. 2.6e-58;
Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 MSDWLTFOKKHLTNTTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Db 7 MQDWLTFOKKHLTNTTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 66

Qy 61 TSEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 67 TSEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 111
```

RESULT 8

```
US-09-961-400-2
; Sequence 2, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-2
```

```
Query Match          98.5%; Score 573; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 4e-58;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 DWLTFQKKHLTNTTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 62
Db 2 DWLTFQKKHLTNTTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 61
```

```
Db 1 MSDWLTFOKKHLTNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAICKGIIASKNVLT 60
QY 61 TSEFVLSDCNVTSPCKYKLLKXSTNTFCVTCENQAPVHFVGHC 105
Db 61 TSEFVLSDCNVTSPCKYKLLKXSTNTFCVTCENQAPVHFVGHC 105

RESULT 2
US-09-961-400-13
; Sequence 13, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-13

Query Match 100.0%; Score 582; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.7e-59;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDWLTFOKKHLTNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAICKGIIASKNVLT 60
Db 1 MSDWLTFOKKHLTNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAICKGIIASKNVLT 60

QY 61 TSEFVLSDCNVTSPCKYKLLKXSTNTFCVTCENQAPVHFVGHC 105
Db 61 TSEFVLSDCNVTSPCKYKLLKXSTNTFCVTCENQAPVHFVGHC 105

RESULT 3
US-09-948-391A-6
; Sequence 6, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant)
; OTHER INFORMATION: Met (-1) RALRL1
US-09-948-391A-6

Query Match 99.3%; Score 578; DB 10; Length 105;
Best Local Similarity 99.0%; Pred. No. 1.1e-58;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSDWLTFOKKHLTNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAICKGIIASKNVLT 60
Db 1 MQDWLTFOKKHLTNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAICKGIIASKNVLT 60

QY 61 TSEFVLSDCNVTSPCKYKLLKXSTNTFCVTCENQAPVHFVGHC 105
Db 61 TSEFVLSDCNVTSPCKYKLLKXSTNTFCVTCENQAPVHFVGHC 105

RESULT 4
US-09-961-400-6
; Sequence 6, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-6

Query Match 99.3%; Score 578; DB 10; Length 105;
Best Local Similarity 99.0%; Pred. No. 1.1e-58;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSDWLTFOKKHLTNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAICKGIIASKNVLT 60
Db 1 MQDWLTFOKKHLTNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAICKGIIASKNVLT 60

QY 61 TSEFVLSDCNVTSPCKYKLLKXSTNTFCVTCENQAPVHFVGHC 105
Db 61 TSEFVLSDCNVTSPCKYKLLKXSTNTFCVTCENQAPVHFVGHC 105

RESULT 5
US-09-948-391A-11
; Sequence 11, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 33.6904 Seconds
(without alignments)
865.070 Million cell updates/sec

Title: US-09-961-400-13

Perfect score: 582

Sequence: 1 MSDWLTQKKHLNTRDVC.....TFCVTCENQAPVHFVGVC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582	100.0	105	10	US-09-948-391A-13
2	582	100.0	105	10	US-09-961-400-13
3	578	99.3	105	10	US-09-948-391A-6
4	578	99.3	105	10	US-09-961-400-6
5	577	99.1	104	10	US-09-948-391A-11
6	577	99.1	104	10	US-09-961-400-11
7	575	98.8	111	10	US-09-961-400-9
8	573	98.5	104	10	US-09-961-400-2
9	573	98.5	127	10	US-09-948-391A-28
10	573	98.5	127	10	US-09-961-400-28
11	565	97.1	105	10	US-09-961-400-8
12	564	96.9	104	10	US-09-948-391A-2
13	564	96.9	104	10	US-09-948-391A-4
14	564	96.9	104	10	US-09-961-400-4
15	560	96.2	105	10	US-09-948-391A-8

```

16 560 96.2 111 10 US-09-948-391A-9
17 556 95.5 105 14 US-10-153-882-2
18 551 94.7 104 9 US-09-986-119-1
19 551 94.7 104 10 US-09-918-887-1
20 543 93.3 104 12 US-10-461-713-53
21 445 76.5 83 9 US-09-986-119-3
22 445 76.5 83 10 US-09-918-887-3
23 285.5 49.1 111 10 US-09-948-391A-26
24 285.5 49.1 111 10 US-09-961-400-26
25 281.5 48.4 111 10 US-09-961-400-17
26 280.5 48.2 110 10 US-09-948-391A-24
27 280.5 48.2 110 10 US-09-961-400-24
28 277.5 47.7 111 10 US-09-948-391A-21
29 277.5 47.7 111 10 US-09-961-400-21
30 277.5 47.7 111 10 US-09-948-391A-22
31 277.5 47.7 117 10 US-09-961-400-22
32 276.5 47.5 110 10 US-09-948-391A-15
33 276.5 47.5 110 10 US-09-961-400-15
34 275.5 47.3 111 10 US-09-948-391A-17
35 272.5 46.8 110 10 US-09-961-400-19
36 266.5 45.8 110 10 US-09-948-391A-19
37 157.5 27.1 169 13 US-10-016-447-2
38 144 24.7 119 12 US-10-016-248-89
39 144 24.7 119 15 US-10-074-978A-139
40 128.5 22.1 124 13 US-10-016-447-5
41 125 21.5 124 12 US-10-037-417-103
42 113 19.4 147 9 US-09-286-240-6
43 113 19.4 147 9 US-09-863-777-2
44 113 19.4 147 9 US-09-731-872-254
45 113 19.4 147 10 US-09-876-997-254

```

ALIGNMENTS

RESULT 1

```

US-09-948-391A-13
; Sequence 13, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 and Gln2Ser
; OTHER INFORMATION: substitution (recombinant Met(-1) RnPLR1 Q1S)
US-09-948-391A-13

```

Query Match 100.0%; Score 582; DB 10; Length 105;

Best Local Similarity 100.0%; Pred. No. 3.7e-59;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDWLTQKKHLNTRDVCNNIMSTNLFHCCKNTFYSRPEVKAICGIIASKNVLT 60

|||||

```
/ TELEFAX: 201-912-0442
/ TELEX: No. 572805 Applicable
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 104 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: N
/ ANTI-SENSE: N
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Rana pipiens
/ DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-1

Query Match      94.7%; Score 551; DB 1; Length 104;
Best Local Similarity 96.1%; Pred. No. 1.5e-59;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 DMLTFQKKHLINTRDVCNNIMSTNLFHCKDKNTFIYSRPVPVKAICKGIIRASKNVLTTTS 62
Db      2 DMLTFQKKHLINTRDVCNNIMSTNLFHCKDKNTFIYSRPVPVKAICKGIIRASKNVLTTTS 61

QY      63 EFYLSDCNVTSPCKYKIKKSTNTFCVTCENQAPVHFVGVGHC 105
Db      62 EFYLSDCNVTSPCKYKIKKSTNTFCVTCENQAPVHFVGVGSC 104
```

Search completed: May 7, 2004, 21:40:44
Job time : 12.1796 secs

;/ FILING DATE: 13-NOV-1989
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Jay, Mark H.
;/ REGISTRATION NUMBER: 27507
;/ REFERENCE/DOCKET NUMBER: 5006 US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 718-625-0399
;/ TELEFAX: 718-625-0399
;/ TELEX: No. 5529775 Applicable
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 104 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ HYPOTHETICAL: N
;/ ANTI-SENSE: N
;/ FRAGMENT TYPE: N-terminal
;/ ORIGINAL SOURCE:
;/ ORGANISM: Rana pipiens
;/ DEVELOPMENTAL STAGE: Embryo
;/ US-08-283-971-1

Query Match 94.7%; Score 551; DB 1; Length 104;
Best Local Similarity 96.1%; Pred. No. 1.5e-59;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 DLTFFQKKHLNTRDVCNINMSTNLFHCKDKNTFIYSRPEVKAICKGIASKNVLTTTS 62
Db 2 DLTFFQKKHLNTRDVCNINMSTNLFHCKDKNTFIYSRPEVKAICKGIASKNVLTTTS 61

QY 63 EFLYSDCNVTSRCPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 105
Db 62 EFLYSDCNVTSRCPCKYKLLKSTNFCVTCENQAPVHFVGVGSC 104

RESULT 14

;/ Sequence 1, Application US/07921619
;/ Patent No. 5595734
;/ GENERAL INFORMATION:
;/ APPLICANT: Ardelt Ph.D, Wojciech J.
;/ APPLICANT: Mikulski, Stanislaw M.
;/ TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
;/ NUMBER OF SEQUENCES: 1
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Mark H. Jay, P.C.
;/ STREET: P.O. Box 020083, General Post Office
;/ CITY: Brooklyn
;/ STATE: New York
;/ COUNTRY: USA
;/ ZIP: 11202-0002
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.24
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/07/921,619
;/ FILING DATE: 19920728
;/ CLASSIFICATION: 530
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/178,118
;/ FILING DATE: 06-APR-1988
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/436,141
;/ FILING DATE: 13-NOV-1989
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Jay, Mark H.
;/ REGISTRATION NUMBER: 27507
;/ REFERENCE/DOCKET NUMBER: 5005 US
;/ TELECOMMUNICATION INFORMATION:

;/ TELEPHONE: 718-625-0399
;/ TELEFAX: 718-625-0399
;/ TELEX: No. 5595734 Applicable
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 104 amino acids
;/ TYPE: AMINO ACID
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ HYPOTHETICAL: N
;/ ANTI-SENSE: N
;/ FRAGMENT TYPE: N-terminal
;/ ORIGINAL SOURCE:
;/ ORGANISM: Rana pipiens
;/ DEVELOPMENTAL STAGE: Embryo
;/ US-07-921-619-1

Query Match 94.7%; Score 551; DB 1; Length 104;
Best Local Similarity 96.1%; Pred. No. 1.5e-59;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 DLTFFQKKHLNTRDVCNINMSTNLFHCKDKNTFIYSRPEVKAICKGIASKNVLTTTS 62
Db 2 DLTFFQKKHLNTRDVCNINMSTNLFHCKDKNTFIYSRPEVKAICKGIASKNVLTTTS 61

QY 63 EFLYSDCNVTSRCPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 105
Db 62 EFLYSDCNVTSRCPCKYKLLKSTNFCVTCENQAPVHFVGVGSC 104

RESULT 15

;/ US-08-467-955-1
;/ Sequence 1, Application US/08467955
;/ Patent No. 5728805
;/ GENERAL INFORMATION:
;/ APPLICANT: Ardelt Ph.D, Wojciech J.
;/ TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
;/ NUMBER OF SEQUENCES: 2
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Mark H. Jay, P.A.
;/ STREET: P.O. Box E
;/ CITY: Short Hills
;/ STATE: New Jersey
;/ COUNTRY: USA
;/ ZIP: 07078-0383
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.24
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/467,955
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/178,118
;/ FILING DATE: 06-APR-1988
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/436,141
;/ FILING DATE: 13-NOV-1989
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/814,332
;/ FILING DATE: 03-FEB-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/283,970
;/ FILING DATE: 01-AUG-1994
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Jay, Mark H.
;/ REGISTRATION NUMBER: 27507
;/ REFERENCE/DOCKET NUMBER: 5007 US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 201-912-9066

APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-51

Query Match 95.5%; Score 556; DB 3; Length 358;
Best Local Similarity 95.2%; Pred. No. 1.9e-59;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 MSDWLTFOKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLT 60
DB 1 MEDWLTFOKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLT 60
QY 61 TSEFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVGHC 105
DB 61 TSEFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVGSC 105

RESULT 12
US-08-875-811-26
Sequence 26, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-26

Query Match 95.4%; Score 555; DB 3; Length 105;
Best Local Similarity 95.2%; Pred. No. 5e-60;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 MSDWLTFOKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLT 60
DB 1 MSDWLTFOKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLT 60
QY 61 TSEFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVGHC 105
DB 61 TSEFYLSDCNVTSPCKYKLLKSTNTFCVTENQAPVHFVGVGSC 105

RESULT 13
US-08-283-971-1
Sequence 1, Application US/08283971
Patent No. 5529775
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141

```
; DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match          95.5%; Score 556; DB 1; Length 104;
Best Local Similarity 97.1%; Pred. No. 3.7e-60;
Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 DMLTFQKKHINTRDVDCNNIMSTNLFHCKDKNTFIYSRPFVKAICKGIITASKNVLTTS 62
Db 2 DMLTFQKKHINTRDVDCNNIMSTNLFHCKDKNTFIYSRPFVKAICKGIITASKNVLTTS 61

QY 63 EYFLSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 62 EYFLSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 9
US-08-875-811-39
; Sequence 39, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; OPERATING SYSTEM: PC-DOS/MS-DOS
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-39

Query Match          95.5%; Score 556; DB 3; Length 105;
Best Local Similarity 95.2%; Pred. No. 3.8e-60;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSDWLFQKKHINTRDVDCNNIMSTNLFHCKDKNTFIYSRPFVKAICKGIITASKNVLT 60
Db 1 MEDWLFQKKHINTRDVDCNNIMSTNLFHCKDKNTFIYSRPFVKAICKGIITASKNVLT 60

QY 61 TSEFYLSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
```

```
Db 61 TSEFYLSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 10
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; OPERATING SYSTEM: PC-DOS/MS-DOS
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-41

Query Match          95.5%; Score 556; DB 3; Length 355;
Best Local Similarity 95.2%; Pred. No. 1.8e-59;
Matches 100; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSDWLFQKKHINTRDVDCNNIMSTNLFHCKDKNTFIYSRPFVKAICKGIITASKNVLT 60
Db 251 MEDWLFQKKHINTRDVDCNNIMSTNLFHCKDKNTFIYSRPFVKAICKGIITASKNVLT 310

QY 61 TSEFYLSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 311 TSEFYLSDCNVTSRPPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 355

RESULT 11
US-08-875-811-51
; Sequence 51, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
```

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..355
; OTHER INFORMATION: /note="E6FB[Met-(-1)]SerrOnc"
US-08-875-811-64

Query Match 96.2%; Score 560; DB 3; Length 355;
Best Local Similarity 96.2%; Pred. No. 6e-60;
Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIIASKNVLT 60
Db 251 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIIASKNVLT 310

Qy 61 TSEFYSLDCNVTSPCKYKLLKSKTNTFCVTCENQAPVHFVGVGHC 105
Db 311 TSEFYSLDCNVTSPCKYKLLKSKTNTFCVTCENQAPVHFVGVGSC 355

RESULT 7
US-08-875-811-55
; Sequence 55, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid

TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-55

Query Match 96.2%; Score 560; DB 3; Length 366;
Best Local Similarity 96.2%; Pred. No. 6.2e-60;
Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIIASKNVLT 60
Db 262 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSPPEPVKAICKGIIASKNVLT 321

Qy 61 TSEFYSLDCNVTSPCKYKLLKSKTNTFCVTCENQAPVHFVGVGHC 105
Db 322 TSEFYSLDCNVTSPCKYKLLKSKTNTFCVTCENQAPVHFVGVGSC 366

RESULT 8
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-49

Query Match 96.2%; Score 560; DB 3; Length 355;
Best Local Similarity 96.2%; Pred. No. 6e-60;
Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSDWLTQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
DB 251 MSDWLTQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 310
QY 61 TSEFYLSDCNVTSRCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
DB 311 TSEFYLSDCNVTSRCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 355

RESULT 5
US-08-875-811-57
Sequence 57, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811

FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-57

Query Match 96.2%; Score 560; DB 3; Length 355;
Best Local Similarity 96.2%; Pred. No. 6e-60;
Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSDWLTQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
DB 1 MSDWLTQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
QY 61 TSEFYLSDCNVTSRCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
DB 61 TSEFYLSDCNVTSRCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 105

RESULT 6
US-08-875-811-64
Sequence 64, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US

Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVL 60
Db 8 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVL 67
Qy 61 TSEFYSDCNVTSRPFCKYKLLKSKSTNTFCVTCENQAPVHFVGVGHC 105
Db 68 TSEFYSDCNVTSRPFCKYKLLKSKSTNTFCVTCENQAPVHFVGVGSC 112

RESULT 2

US-08-875-811-59
; Sequence 59, Application US/08875811
; Patent No. 6045793

; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís

; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins

; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811

; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 19-FEB-1997

; FILING DATE: 19-FEB-1997
; APPLICATION NUMBER: US 60/011,800

; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.

; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-875-811-59

Query Match 96.2%; Score 560; DB 3; Length 251;
Best Local Similarity 96.2%; Pred. No. 3.8e-60;

Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVL 60
Db 147 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVL 206
Qy 61 TSEFYSDCNVTSRPFCKYKLLKSKSTNTFCVTCENQAPVHFVGVGHC 105
Db 207 TSEFYSDCNVTSRPFCKYKLLKSKSTNTFCVTCENQAPVHFVGVGSC 251

RESULT 3

US-08-875-811-61

; Sequence 61, Application US/08875811
; Patent No. 6045793

; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís

; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins

; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811

; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588

; FILING DATE: 19-FEB-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800

; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.

; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-875-811-61

Query Match 96.2%; Score 560; DB 3; Length 254;
Best Local Similarity 96.2%; Pred. No. 3.9e-60;

Matches 101; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVL 60
Db 1 MSDWLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVL 60
Qy 61 TSEFYSDCNVTSRPFCKYKLLKSKSTNTFCVTCENQAPVHFVGVGHC 105
Db 61 TSEFYSDCNVTSRPFCKYKLLKSKSTNTFCVTCENQAPVHFVGVGSC 105

RESULT 4

US-08-875-811-49

; Sequence 49, Application US/08875811
; Patent No. 6045793

; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís

; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins

; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:28:45 ; Search time 12.1796 Seconds
(without alignments)
445.066 Million cell updates/sec

Title: US-09-961-400-13
Perfect score: 582
Sequence: 1 MSDWLFQKHLNTRDVC.....TFVCVCNQAPVHFVGVC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560	96.2	112	3	US-08-875-811-32
2	560	96.2	251	3	US-08-875-811-59
3	560	96.2	254	3	US-08-875-811-61
4	560	96.2	355	3	US-08-875-811-49
5	560	96.2	355	3	US-08-875-811-57
6	560	96.2	355	3	US-08-875-811-64
7	560	96.2	366	3	US-08-875-811-55
8	556	95.5	104	1	US-08-467-955-2
9	556	95.5	105	3	US-08-875-811-39
10	556	95.5	355	3	US-08-875-811-41
11	556	95.5	358	3	US-08-875-811-51
12	555	95.4	105	3	US-08-875-811-26
13	551	94.7	104	1	US-08-283-971-1
14	551	94.7	104	1	US-07-921-619-1
15	551	94.7	104	1	US-08-467-955-1
16	551	94.7	104	2	US-08-891-848-13
17	551	94.7	104	3	US-08-875-811-1
18	551	94.7	104	3	US-09-394-268-1
19	551	94.7	104	4	US-09-071-672-1
20	551	94.7	104	4	US-09-687-748-1
21	551	94.7	104	4	US-08-626-288-1
22	551	94.7	104	4	US-09-095-429-1
23	551	94.7	104	4	US-09-986-119-1
24	551	94.7	106	3	US-08-875-811-28
25	551	94.7	107	3	US-08-875-811-30
26	551	94.7	129	3	US-08-875-811-63
27	551	94.7	358	3	US-08-875-811-45

28 551 94.7 365 3 US-08-875-811-53
29 551 94.7 379 3 US-08-875-811-43
30 549 94.3 105 3 US-08-875-811-24
31 548 94.2 104 4 US-08-626-288-2
32 548 94.2 104 4 US-09-095-429-2
33 543 93.3 104 3 US-09-394-268-2
34 543 93.3 104 4 US-09-687-748-2
35 532 91.4 107 3 US-08-875-811-20
36 499 85.7 360 3 US-08-875-811-47
37 484.5 83.2 111 3 US-08-875-811-22
38 445 76.5 83 4 US-08-875-811-22
39 445 76.5 83 4 US-09-071-672-3
40 445 76.5 83 4 US-09-986-119-3
41 287 49.3 111 2 US-08-851-848-12
42 287 49.3 111 3 US-08-875-811-8
43 216.5 37.2 114 3 US-09-223-118-4
44 204.5 35.1 114 3 US-09-223-118-2
45 203.5 35.0 114 3 US-09-223-118-1

ALIGNMENTS

RESULT 1
US-08-875-811-32
; Sequence 32, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-32
Query Match 96.2%; Score 560; DB 3; Length 112;
Best Local Similarity 96.2%; Pred. No. 1.3e-60;

Search completed: May 11, 2004, 14:35:05
Job time : 11.0452 secs

ID	RNR_AX1PR	STANDARD;	PRT;	151 AA.
AC	P87350;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DT	Ribonuclease, brain (EC 3.1.27.-) (BRB).			
GN	BRN.			
OS	Axis porcinus (Hog deer).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;			
OC	Cervidae; Cervinae; Axis.			
OX	NCBI_TaxID=57737;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=98278842; PubMed=9611269;			
RX	Breukelman H.J.; van der Munnik N.; Kleineidam R.G.; Furia A.,			
RA	Beintema J.J.;			
RA	"Secretory ribonuclease genes and pseudogenes in true ruminants.";			
RL	Gene 212:259-268 (1998).			
RT	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC				
CC	EMBL; Y11670; CAA72368.1; -.			
DR	HSSP; P00656; ISRN.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; rnasea; 1.			
DR	PRINTS; PR00794; RIBONUCLEASE.			
DR	ProDom; PD000535; RNaseA; 1.			
DR	SMART; SM00092; RNaseA; 1.			
DR	PROSITE; PS00127; RNASE PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease; Glycoprotein.			
FT	ACT_SITE 41 41			
FT	DISULFID 26 84			
FT	DISULFID 40 95			
FT	DISULFID 58 110			
FT	DISULFID 65 72			
FT	CARBOHYD 62 62			
FT	CARBOHYD 129 129			
FT	CARBOHYD 133 133			
FT	SEQUENCE 151 AA; 16819 MW; E95F3757FFC5B233 CRC64;			
SEQ				
Query Match				
Best Local Similarity 21.0%; Score 127.5; DB 1; Length 151;				
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;				
QY	5	ATFOQRHI-----INTPIICNTIMDNNIYIVGGCKRVNFTFISSATTTKAICTGVINM 58		
Db	6	AKPRRHM DAGSSSGNSNYCNQMKRR -RWTGRCCKPVNIFVHESLDSVKAVCS---QK 61		
QY	59	NVL-----STTRFOLNCTRTSITPRP-CPYSSRRTETNYICVKCE-NQY-PVHFA 105		
Db	62	NITCKNGQPCNVCQSNSTMNITDCRETGSSKYPNCAYKTSQKQYITVACEGNPVVPVHFD 121		
QY	106	G 106		
Db	122	G 122		
RESULT 15				
RNP_IGUG	ID	RNP_IGUG	STANDARD;	PRT; 119 AA.
AC	P80287;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			

QY 59 NVL-----SITRQLNCTWTSTTPRP-CPYSSRTETNYICVKCENQ--YPVVHF 120
 DB 62 NITCKNGPNCYQSNSTNMTIDCRQTGSSKYPNCAYKTSQKQYITVACBGDPYPVPHF 120

RESULT 12
 ANGE2_BOVIN STANDARD; PRT; 123 AA.
 ID ANGE2_BOVIN STANDARD; PRT; 123 AA.
 AC P80929;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin-2 (EC 3.1.1.27.-).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 GN [1]
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Milk, and Serum;
 RX MEDLINE=97409980; PubMed=9266695;
 RA Struydom D.J., Bond M.D., Vallee B.L.;
 RT "An angiotensin protein from bovine serum and milk -- purification and
 RL primary structure of angiotensin-2.";
 RL Eur. J. Biochem. 247:535-544 (1997).
 CC -!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and
 CC has very low ribonuclease activity. Has potent angiogenic
 CC activity. Angiotensin induces vascularization of normal and
 CC malignant tissues. Abolishes protein synthesis by specifically
 CC hydrolyzing cellular tRNAs.
 CC -!- TISSUE SPECIFICITY: Serum and milk.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR HSSP; P10152; IAGI.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Glycoprotein;
 KW Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
 FT ACT_SITE 12 12 BY SIMILARITY.
 FT ACT_SITE 39 39 BY SIMILARITY.
 FT ACT_SITE 113 113 BY SIMILARITY.
 FT DISULFID 25 80
 FT DISULFID 38 91
 FT DISULFID 56 106
 FT CARBOHYD 33 33 N-LINKED (GLCNAC...).
 SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 21.0%; Score 127.5; DB 1; Length 123;
 Best Local Similarity 30.6%; Pred. No. 6.8e-07;
 Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5

QY 7 FQCKHIINTPI-----ICNTIMNNIYVGCGCKRWFTFISSATVKAIC---TGVINM 58
 DB 8 FLRKHVDFSPQTGHDDRYCNTMERR--NMTRPCDKTNTFIHNSDDIRAVCDRNGEYR 65

QY 59 NVLSITR--FQLNCTRTSITPR-PCPYSSRTETNYICVKCENQYPVH 103
 DB 66 NGLRSRPFQVTTCHRGSGSPRCPRYAFRANKRVIVIRCDRGPFH 113

RESULT 13
 RNER_GIRCA STANDARD; PRT; 141 AA.
 ID RNER_GIRCA STANDARD; PRT; 141 AA.
 AC Q29542; Q29533;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)

Matches	38;	Conservative	17;	Mismatches	43;	Indels	23;	Gaps	7;
---------	-----	--------------	-----	------------	-----	--------	-----	------	----

QY	5	ATPQKH	-----INTPI	CNTIMDNNIYVGGQCKRVNTFTI	SSATTVKAICTGV	INM	58
		:	:	:	:	:	
Db	32	AKFRQHMD	SGSSSSPNYC	QMCKRR-RMTHGR	CKPVNTFVHESL	DDVKVCS	---QX 87
		:	:	:	:	:	
QY	59	NVL-----	STTRFQ	LNTCTRTSITPRP-CPYSS	RTETNYICVKCB-NQY	PVHPA	105
		:	:	:	:	:	
Db	88	NITCKNGHP	NCYQSKTMSITD	CRETGSSKYPNCAYKTSQ	KQYITVACEG	NPVPVHF	147
		:	:	:	:	:	
QY	106	G	106				
		:	:	:	:	:	
Db	148	G	148				
		:	:	:	:	:	

RESULT 10	
RNP_PIG	STANDARD; PRT; 124 AA.
ID	RNP_PIG
AC	P00671;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
GN	RNASE1 OR RNS1.
OS	Sus scrofa (Pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX	NCBI_TaxID=9823;
RP	[1]
RP	SEQUENCE.
RP	MEDLINE=70104197; PubMed=5460946;
RA	JACKSON R.L., Hirs C.H.W.;
RA	"The primary structure of porcine pancreatic ribonuclease. II. The
RT	amino acid sequence of the reduced S-aminoethylated protein.";
RT	J. Biol. Chem. 245:637-653(1970).
RL	[2]
RP	REVISION TO 2.
RP	Wieringa R.K., Huizinga J.D., Gastra W., Welling G.W., Beintema J.J.;
RA	"Affinity chromatography of porcine pancreatic ribonuclease and
RT	reinvestigation of the N-terminal amino acid sequence.";
RL	FEBS Lett. 31:181-185(1973).
RP	[3]
RP	DISULFIDE BONDS.
RP	MEDLINE=70104198; PubMed=4904878;
RA	Phelan J.J., Hirs C.H.W.;
RT	"The primary structure of porcine pancreatic ribonuclease. 3. The
RT	disulfide bonds.";
RL	J. Biol. Chem. 245:654-661(1970).
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC	with 2', 3'-cyclic phosphate intermediates.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- TISSUE SPECIFICITY: Pancreas.
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR	PIR; A92071; NRPQ.
DR	HSP; P00656; 1SRN.
DR	InterPro; IPR001427; RNaseA.
DR	Pfam; PF00074; rnasea; 1.
DR	PRINTS; PR00794; RIBONUCLEASE.
DR	ProDom; PD000535; RNasea; 1.
DR	SMART; SM00092; RNase Pc; 1.
DR	PROSITE; PS00127; RNASE PANCREATIC; 1.
KW	Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT	DISULFID 26 84
FT	DISULFID 40 95
FT	DISULFID 58 110
FT	DISULFID 65 72
FT	ACT_SITE 12 12
FT	ACT_SITE 41 41
FT	ACT_SITE 119 119
FT	CARBOHYD 21 21
FT	CARBOHYD 34 34
FT	CARBOHYD 76 76

BY SIMILARITY.	
BY SIMILARITY.	
BY SIMILARITY.	
N-LINKED (GLCNAC. . .)	
N-LINKED (GLCNAC. . .)	
N-LINKED (GLCNAC. . .)	

```

DR PIR; A00818; NRWHE.
DR HSP; P00656; 1SRN.
DR InterPro; IP001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase Pc; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 76 N-LINKED (GUCNAC...) (30%).
SQ SEQUENCE 124 AA; 14125 MW; F57475459F697E20 CRC64;

Query Match 22.4%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 9.4e-08;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 7 FQKHII-----NPIIONTMNNIYIVGCKRVNTPFISSATTVAICTGVINMV 60
Db 8 FQKHMDSGNSPNNPNYCNQMMRR-KMTQGRCKPVNTFVHESLEDVRAVCS---QKNV 63
QY 61 I-----STTRFQNTCTRTSITPRP-CPYSSRTETNYCVKCE-NQY-PVHF 104
Db 64 LCKNGRTCYESNTMHTDCRQTGSSKYPNCAYKTSQKEKHIIIVACEGNPVYPVHF 120

RESULT 8
ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995 (1990).
RN [2]_
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length

```

```

RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP PARTIAL SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions.";
RL Biochim. Biophys. Acta 1162:177-186 (1993).
CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC to act on the surface of endothelial cells; once bound,
CC angiogenin is endocytosed and translocated to the nucleus, thereby
CC promoting the endothelial invasiveness necessary for blood vessel
CC formation. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U22516; AAA91366.1; -.
DR EMBL; BC055355; AAH5355.1; -.
DR PIR; A35932; A35932.
DR HSP; P03950; 1A4Y.
DR MGD; MGI:88022; Ang.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase Pc; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
DR Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT CHAIN 1 24
FT SIGNAL 25 145
FT MOD_RES 25 25
FT ANGIOGENIN.
FT PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;

Query Match 22.4%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 1.1e-07;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 34 CKRVNTPFISSATTVAICTGVINMV-ISTTRFQNTCTRTSITPR-PCPYSSRTE 88
Db 63 CKDVTTFHGNKSIKAIKANGSPYRENLRMSKSPFQVTTCKTGSPRPCCQYRASAG 122
QY 89 TNYICVKCENQYPVHF 104
Db 123 FRHVIACENGLPVHF 138

RESULT 9
RNBR_BOVIN STANDARD; PRT; 167 AA.
ID RNBR_BOVIN
AC P39873;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

```

```

RT developmentally regulated genes when expressed in NIH 3T3
RT fibroblasts."
RL Mol. Cell. Biol. 17:1503-1512(1997).
CC -!- FUNCTION: Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs (By similarity).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U22519; AAA91367.1; --
DR HSP; P03950; IAA4.
DR MGD; MGI:104984; Angrp.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR Signal; Hydrolase; Nuclease; Endonuclease;
KW Pyrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
FT SEQUENCE 145 AA; 16696 MW; 16696 MW; DE9D3BC92F1D682C CRC64;
Query Match 25.5%; Score 154.5; DB 1; Length 145;
Best Local Similarity 43.6%; Pred. No. 1e-09;
Matches 34; Conservative 12; Mismatches 23; Indels 9; Gaps 4;
QY 34 CKRVNFIISATTVKAIC-----TGVINNVLSSTRFQNLNCTRTSITPR-PCPYSSR 86
Db 63 CKEVNFIHDTKKNKAICGNGRPGV-NPRI-SNSRFQVTTCTHKGSPRPCCYNAF 120
QY 87 TETNYICVKCNQYVPHF 104
Db 121 KQFYIVVACEDGMPVHF 138
RESULT 6
ID ANGR_MOUSE STANDARD; PRT; 145 AA.
AC Q64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=86079109; PubMed=8530072;
RA Brown W.E., Nobile V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RT protein gene and two pseudogenes."
RL Genomics 29:200-206(1995).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U22519; AAA91367.1; --
DR HSP; P03950; IAA4.
DR MGD; MGI:104984; Angrp.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR Signal; Hydrolase; Nuclease; Endonuclease;
KW Pyrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
FT SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4D CRC64;
Query Match 24.7%; Score 149.5; DB 1; Length 145;
Best Local Similarity 43.4%; Pred. No. 3.5e-09;
Matches 33; Conservative 10; Mismatches 28; Indels 5; Gaps 3;
QY 34 CKRVNFIISATTVKAIC--TGVINNV-LSTRFQNLNCTRTSITPR-PCPYSSRTE 88
Db 63 CKDVFTHDTKKNKAICGKSPYGRNLRISKRFQVTTCTHKGSPRPCCYRASKG 122
QY 89 TNYICVKCNQYVPHF 104
Db 123 FRYIIIGCENGWVPHF 138
RESULT 7
ID RNP_BALAC STANDARD; PRT; 124 AA.
AC P00673;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Balaenoptera acutorostrata (Minke whale) (lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Balaenoptera.
OX NCBI_TaxID=9767;
RN [1]
RP SEQUENCE.
RX MEDLINE=76277855; PubMed=962870;
RA Emmens M., Welling G.W., Beintema J.J.;
RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
RT ribonuclease."
RL Biochem. J. 157:317-323(1976).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

```

RL J. Biochem. 106:729-735(1989).
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC PIR: JX0085; JX0085.
 DR HSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase Pc; 1.
 DR PROSITE: PS00127; RNASE PANCREATIC; 1.
 DR KX Hydroxylase; Nuclease; Endonuclease; 3D-structure;
 KW Pyroliadone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35 BY SIMILARITY.
 FT ACT_SITE 104 104 BY SIMILARITY.
 FT DISULFID 19 72 BY SIMILARITY.
 FT DISULFID 34 82 BY SIMILARITY.
 FT DISULFID 52 97 BY SIMILARITY.
 FT DISULFID 94 111 PROBABLE.
 SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;
 Query Match 60.9%; Score 369; DB 1; Length 111;
 Best Local Similarity 65.5%; Pred. No. 6.4e-33;
 Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;
 QY 3 NWATFOQKHIIINPPII-CNTIMDNNTIYVGQCKRVNTFIISATVKAICTGVI-MNMV 60
 Db 2 NNAKFEKHIRSTSDICNTIMDKAIYVGKCKERTFIISSEDNVKAICSGVSPDRKE 61
 QY 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRC 110
 Db 62 LSTTSFKLNTCTRTSITPRPCPYSPDNKKICVKCKQLPVHFGVIGRC 111
 RESULT 4
 ID RN30_RANPI STANDARD; PRT; 104 AA.
 AC P22069;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P-30 protein (EC 3.1.27.-) (Onconase).
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=91093131; PubMed=1985896;
 RA Ardelit W., Mikulski S.M., Shogen K.;
 RT "Amino acid sequence of an anti-tumor protein from Rana pipiens
 RT oocytes and early embryos. Homology to pancreatic ribonucleases.";
 RL J. Biol. Chem. 266:245-251(1991).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=93066156; PubMed=1438177;
 RA Mosimann S.C., Johns K.L., Ardelit W., Mikulski S.M., Shogen K.,
 RA James M.N.G.;
 RT "Comparative molecular modeling and crystallization of p-30 protein:
 RT a novel antitumor protein of Rana pipiens oocytes and early
 RT embryos.";
 RL Proteins 14:392-400(1992).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
 RX MEDLINE=94166079; PubMed=8120892;
 RA Mosimann S.C., Ardelit W., James M.N.G.;
 RT "Refined 1.7 A x-ray crystallographic structure of p-30 protein, an
 RT amphibian ribonuclease with anti-tumor activity.";
 RL J. Mol. Biol. 236:1141-1153(1994).

CC -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity
 CC against several tumor cell lines in vitro, as well as antitumor
 CC in vivo. It exhibits a ribonuclease-like activity against high
 CC molecular weight ribosomal RNA.
 CC -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC PDB; IONC; 31-JAN-94.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase Pc; 1.
 DR PROSITE: PS00127; RNASE PANCREATIC; 1.
 DR KX Hydroxylase; Nuclease; Endonuclease; 3D-structure;
 KW Pyroliadone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 31 31
 FT ACT_SITE 97 97
 FT DISULFID 19 68
 FT DISULFID 30 75
 FT DISULFID 48 90
 FT DISULFID 87 104
 FT HELIX 3 10
 FT STRAND 11 12
 FT HELIX 19 22
 FT STRAND 23 24
 FT TURN 26 30
 FT TURN 33 38
 FT STRAND 41 45
 FT HELIX 46 48
 FT TURN 49 50
 FT TURN 55 58
 FT STRAND 63 70
 FT TURN 74 75
 FT STRAND 77 84
 FT STRAND 86 91
 FT TURN 92 93
 FT STRAND 94 101
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;
 Query Match 45.0%; Score 272.5; DB 1; Length 104;
 Best Local Similarity 49.1%; Pred. No. 1.4e-22;
 Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
 QY 3 NWATFOQKHIIINPPII-CNTIMDNNTIYVGQCKRVNTFIISATVKAICTGVI-MNMV 60
 Db 2 DMWTFQKKTITRDVDCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGLIASKNV 57
 QY 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRC 110
 Db 58 LITSEFYLSDC---NVTSPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 104
 RESULT 5
 ID ANG3_MOUSE STANDARD; PRT; 145 AA.
 AC P97802;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
 DE (BF-5).
 GN ANG3 OR ANGL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=97184476; PubMed=9032278;
 Fu X., Kamps M.P.;
 RT "E2a-Pbx1 induces aberrant expression of tissue-specific and

CC as substrates with a 3' flanking guanine. Hydrolyzes poly(U) and poly(C)
 CC as substrates, and prefers the former. The S-lectins in frog eggs
 CC may be involved in the fertilization and development of the frog
 CC embryo. This lectin agglutinates various animal cells, including
 CC normal lymphocytes, erythrocytes, and fibroblasts of animal and
 CC human origin. It is cytotoxic against several tumor cells.
 CC
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL; AF039104; AAD10702.1; -
 CC PIR; A27121; A27121.
 CC PDB; 1BC4; 28-OCT-98.
 CC PDB; 1M07; 21-JAN-03.
 CC InterPro: IPR001427; RNaseA.
 CC Pfam; PF00074; RNaseA; 1.
 CC ProDom; PD000535; RNaseA; 1.
 CC SMART; SM00092; RNaseA; 1.
 CC PROSITE; PS00127; RNASE PANCREATIC; 1.
 CC KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
 CC KW Signal; Pyrrolidone carboxylic acid.
 CC FT SIGNAL 1 22
 CC FT CHAIN 23 133 RIBONUCLEASE, OOCYTES.
 CC FT MOD RES 23 23 PYRROLIDONE CARBOXYLIC ACID.
 CC FT ACT SITE 32 32
 CC FT ACT SITE 57 57
 CC FT ACT SITE 125 125
 CC FT DISULFID 41 93
 CC FT DISULFID 56 103
 CC FT DISULFID 74 118
 CC FT DISULFID 115 132
 CC FT HELIX 25 32
 CC FT HELIX 41 45
 CC FT TURN 48 49
 CC FT STRAND 59 63
 CC FT HELIX 67 73
 CC FT TURN 74 74
 CC FT STRAND 79 84
 CC FT STRAND 90 95
 CC FT STRAND 105 110
 CC FT STRAND 114 119
 CC FT TURN 120 121
 CC FT STRAND 122 129
 CC SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 96.8%; Score 586.5; DB 1; Length 133;
 Best Local Similarity 99.1%; Pred. No. 3.1e-56;
 Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 3 NWATFOQKHINTPII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNVNL 61
 Db 24 NWATFOQKHINTPII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNVNL 83
 Qy 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111
 Db 84 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 133

RESULT 2
 LECS_RANJA STANDARD; PRT; 111 AA.
 ID -RANJA
 AC P18839;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Sialic acid-binding lectin (EC 3.1.1.27.-).
 OS Rana japonica (Japanese reddish frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE=Egg;
 RX MEDLINE=91035319; PubMed=2229005;
 RA Kaniya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
 RA Takayanagi Y., Titani K.;
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
 RL eggs.";
 RL J. Biochem. 108:139-143 (1990).
 CC -!- FUNCTION: The S-lectins in frog eggs may be involved in the
 CC fertilization and development of the frog embryo. This lectin
 CC preferentially agglutinates a large variety of tumor cells, but it
 CC does not agglutinate non-transformed cells and erythrocytes.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC
 CC PIR; JX0120; JX0120.
 CC HSSP; P11916; 1BC4.
 CC InterPro; IPR001427; RNaseA.
 CC Pfam; PF00074; RNaseA; 1.
 CC ProDom; PD000535; RNaseA; 1.
 CC SMART; SM00092; RNaseA; 1.
 CC PROSITE; PS00127; RNASE PANCREATIC; 1.
 CC KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin;
 CC KW Pyrrolidone carboxylic acid.
 CC FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 CC FT ACT SITE 10 10 BY SIMILARITY.
 CC FT ACT SITE 35 35 BY SIMILARITY.
 CC FT ACT SITE 104 104 BY SIMILARITY.
 CC FT DISULFID 19 72
 CC FT DISULFID 34 82
 CC FT DISULFID 52 97
 CC FT DISULFID 94 111
 CC SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 74.3%; Score 450; DB 1; Length 111;
 Best Local Similarity 78.2%; Pred. No. 1.2e-41;
 Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

Qy 3 NWATFOQKHINTP-IICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGV-INNV 60
 Db 2 NWATFOQKHINTP-NTIMDNIIYVGQCKRVNTFISSATTVKAICTGSTRNV 61
 Qy 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
 Db 62 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 111

RESULT 3
 RNPL_RANCA STANDARD; PRT; 111 AA.
 ID -RNPL_RANCA
 AC P14626;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribonuclease, liver (EC 3.1.1.27.5).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=90130374; PubMed=2613682;
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
 RA Okazaki T., Ohgi K., Irie M.;
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
 RT liver.";

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:24:28 ; Search time 10.0452 Seconds
(without alignments)
575.375 Million cell updates/sec

Title: US-09-961-400-26

Perfect score: 606

Sequence: 1 MSNWATFQKHINTPIICN.....ICVKCNQYPVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	586.5	96.8	133	1	RNPO_RANCA
2	450	74.3	111	1	LECS_RANCA
3	369	60.9	111	1	RNPL_RANCA
4	272.5	45.0	104	1	RN30_RANPI
5	154.5	25.5	145	1	ANG3_MOUSE
6	149.5	24.7	145	1	ANG_MOUSE
7	135.5	22.4	124	1	RNP_BALAC
8	135.5	22.4	145	1	ANGI_MOUSE
9	133.5	22.0	167	1	RNBR_BOVIN
10	132.5	21.9	124	1	RNP_PIG
11	128.5	21.2	151	1	RNBR_CAPCA
12	127.5	21.0	123	1	ANG2_BOVIN
13	127.5	21.0	141	1	RNBR_GIRCA
14	127.5	21.0	151	1	RNBR_AXIPR
15	126.5	20.9	119	1	RNP_IGUIG
16	126.5	20.9	146	1	ANGI_CERAE
17	126.5	20.9	146	1	ANGI_MIOTA
18	125	20.6	146	1	ANGI_SAISC
19	123.5	20.4	143	1	RNBR_SHEEP
20	122.5	20.2	124	1	RNP_ANTAM
21	122	20.1	122	1	RNP_MACRU
22	120.5	19.9	128	1	RNP_MYOCO
23	120.5	19.9	147	1	ANGI_PONPY
24	120.5	19.9	149	1	RNP_MOUSE
25	120	19.8	146	1	ANGI_AOTTR
26	119.5	19.7	123	1	ANGI_PIG
27	118.5	19.6	128	1	RNBP_CAVPO
28	118	19.5	146	1	ANGI_SAGOE
29	117.5	19.4	128	1	RNP_HORSE
30	116.5	19.2	124	1	RNP_CAMDR
31	116.5	19.2	128	1	RNP_PROGU
32	115.5	19.1	119	1	RNS4_BOVIN
33	115.5	19.1	146	1	ANGI_MACMU

ALIGNMENTS

RESULT 1

ID	RNPO_RANCA	STANDARD;	PRT;	133 AA.
AC	P11916; Q9PWR7;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DE	Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).			
DE	binding lectin) (SBL-C).			
GN	RCA.			
OS	Rana catesbeiana (Bull frog).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoldea; Ranidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=98165825; PubMed=9497370;			
RA	Huang H.C., Wang S.C., Ieu Y.J., Lu S.C., Liao Y.D.;			
RT	"The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.			
RT	Tissue distribution, cloning, purification, cytotoxicity, and active			
RT	residues for RNase activity";			
RL	J. Biol. Chem. 273:6395-6401(1998).			
RN	[2]			
RP	SEQUENCE OF 23-133.			
RC	TISSUE=Egg;			
RX	MEDLINE=87299649; PubMed=3304421;			
RA	Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,			
RA	Takayanagi G., Hakomori S.;			
RT	"Amino acid sequence of sialic acid binding lectin from frog (Rana			
RT	catesbeiana) eggs.";			
RL	Biochemistry 26:2189-2194(1987).			
RN	[3]			
RP	CHARACTERIZATION, AND SEQUENCE OF 81-101.			
RX	MEDLINE=92220613; PubMed=1373237;			
RA	Liao Y.-D.;			
RT	"A pyrimidine-guanine sequence-specific ribonuclease from Rana			
RT	catesbeiana (bullfrog) oocytes.";			
RL	Nucleic Acids Res. 20:1371-1377(1992).			
RN	[4]			
RP	CHARACTERIZATION.			
RC	TISSUE=Egg;			
RX	MEDLINE=93192604; PubMed=8448385;			
RA	Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,			
RA	Takayanagi Y., Hakomori S., Titani K.;			
RT	"Ribonuclease activity of sialic acid-binding lectin from Rana			
RT	catesbeiana eggs.";			
RL	Glycobiology 3:37-45(1993).			
RN	[5]			
RP	STRUCTURE BY NMR OF 23-133.			
RX	MEDLINE=98437383; PubMed=9761686;			
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;			
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes			
RT	of Rana catesbeiana (bullfrog).";			
RL	J. Mol. Biol. 283:231-244(1998).			
CC	-I- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine			

P10152 bos taurus
P00666 rangifer ta
P31347 oryctolagus
Q8wn64 papio hamad
P03950 homo sapien
Q8wn68 pan troglod
P00664 capreolus c
P00662 giraffa cam
Q9j1h1 mus musculus
P24717 cricetus
O55004 rattus norv
Q9wt55 acornys cahl

34 114 18.8 148 1 ANGI_BOVIN
35 113.5 18.7 124 1 RNP_RANCA
36 113.5 18.7 125 1 ANGI_RABIT
37 113.5 18.7 146 1 ANGI_PAPHA
38 113 18.6 147 1 ANGI_HUMAN
39 113 18.6 147 1 ANGI_PANTR
40 112.5 18.6 124 1 RNP_CAPCA
41 112.5 18.6 124 1 RNP_GIRCA
42 112.5 18.6 148 1 RNS4_MOUSE
43 111.5 18.4 130 1 RNP_CRILLO
44 111.5 18.4 147 1 RNS4_RAT
45 111.5 18.4 149 1 RNP_ACOCA

; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6)
US-09-948-391A-22

Query Match 98.3%; Score 591; DB 10; Length 117;
Best Local Similarity 98.2%; Pred. No. 2.7e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
DB 9 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 68

QY 62 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
DB 69 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 13
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-22

Query Match 98.3%; Score 591; DB 10; Length 117;
Best Local Similarity 98.2%; Pred. No. 2.7e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
DB 9 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 68

QY 62 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

DB 69 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 14
US-09-948-391A-19
; Sequence 19, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
; OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1
; OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

Query Match 97.3%; Score 585; DB 10; Length 110;
Best Local Similarity 97.2%; Pred. No. 1.2e-58;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
DB 2 NWATFOQKHINTPIICNTILNNDNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61

QY 62 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
DB 62 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 15
US-09-948-391A-11
; Sequence 11, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 104


```

; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match          99.3%; Score 597; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.2e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
Db  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61

QY  62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPFHAGIGRCP 110
Db  62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPFHAGIGRCP 110

RESULT 6
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-15

Query Match          99.3%; Score 597; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.2e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
Db  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61

QY  62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPFHAGIGRCP 110
Db  62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPFHAGIGRCP 110

RESULT 7
US-09-961-400-17

```

```

; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-17

Query Match          99.3%; Score 597; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 5.3e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
Db  3  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 62

QY  62  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPFHAGIGRCP 110
Db  63  TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPFHAGIGRCP 111

RESULT 8
US-09-961-400-19
; Sequence 19, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-19

Query Match          98.3%; Score 591; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 2.5e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  2  NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
Db  2  NWATFOQKHINTPIICNTILNDNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61

```

```
Db 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVL 60
Qy 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110

RESULT 2
US-09-961-400-24
; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-24

Query Match 100.0%; Score 601; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVL 60
Db 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVL 60
Qy 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110

RESULT 3
US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RacOR1 Q1S)
US-09-948-391A-26

Query Match 100.0%; Score 601; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVL 60
Db 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVL 61
Qy 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 4
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

Query Match 100.0%; Score 601; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVL 60
Db 2 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVL 61
Qy 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 5
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:34:38 ; Search time 37.8281 Seconds
(without alignments)
807.135 Million cell updates/sec

Title: US-09-961-400-24
Perfect score: 601
Sequence: 1 SNWATFQKHINTPICNT.....ICVKCNQYVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277565755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	601	100.0	110	10	US-09-948-391A-24
2	601	100.0	110	10	US-09-961-400-24
3	601	100.0	111	10	US-09-948-391A-26
4	601	100.0	111	10	US-09-961-400-26
5	597	99.3	110	10	US-09-948-391A-15
6	597	99.3	110	10	US-09-961-400-15
7	597	99.3	111	10	US-09-961-400-17
8	591	98.3	111	10	US-09-961-400-19
9	591	98.3	111	10	US-09-948-391A-17
10	591	98.3	111	10	US-09-948-391A-21
11	591	98.3	111	10	US-09-961-400-21
12	591	98.3	117	10	US-09-948-391A-22
13	591	98.3	117	10	US-09-961-400-22
14	585	97.3	110	10	US-09-948-391A-19
15	280.5	46.7	104	10	US-09-948-391A-11

16	280.5	46.7	104	10	US-09-961-400-11	Sequence 11, Appl
17	280.5	46.7	105	10	US-09-948-391A-13	Sequence 13, Appl
18	280.5	46.7	105	10	US-09-961-400-13	Sequence 13, Appl
19	276.5	46.0	104	10	US-09-961-400-2	Sequence 2, Appl
20	276.5	46.0	105	10	US-09-948-391A-6	Sequence 6, Appl
21	276.5	46.0	105	10	US-09-961-400-6	Sequence 6, Appl
22	276.5	46.0	127	10	US-09-948-391A-28	Sequence 28, Appl
23	276.5	46.0	127	10	US-09-961-400-28	Sequence 28, Appl
24	275.5	45.8	104	10	US-09-948-391A-2	Sequence 2, Appl
25	273.5	45.5	111	10	US-09-961-400-9	Sequence 9, Appl
26	272.5	45.3	104	9	US-09-986-119-1	Sequence 1, Appl
27	272.5	45.3	104	10	US-09-918-887-1	Sequence 1, Appl
28	272.5	45.3	105	14	US-10-153-882-2	Sequence 2, Appl
29	270.5	45.0	104	10	US-09-948-391A-4	Sequence 4, Appl
30	270.5	45.0	104	10	US-09-961-400-4	Sequence 4, Appl
31	270.5	45.0	105	10	US-09-961-400-8	Sequence 8, Appl
32	264.5	44.0	104	12	US-10-461-713-53	Sequence 53, Appl
33	261.5	43.5	105	10	US-09-948-391A-8	Sequence 8, Appl
34	261.5	43.5	111	10	US-09-948-391A-9	Sequence 9, Appl
35	206	34.3	83	9	US-09-986-119-3	Sequence 3, Appl
36	206	34.3	83	10	US-09-918-887-3	Sequence 3, Appl
37	158	26.3	169	13	US-10-016-447-2	Sequence 2, Appl
38	135.5	22.5	124	12	US-10-037-417-103	Sequence 103, App
39	126.5	21.0	119	12	US-10-016-248-89	Sequence 89, Appl
40	126.5	21.0	119	15	US-10-074-978A-139	Sequence 139, App
41	121	20.1	99	15	US-10-074-978A-141	Sequence 141, App
42	117.5	19.6	124	12	US-10-461-713-52	Sequence 52, Appl
43	117	19.5	147	9	US-09-731-872-254	Sequence 254, App
44	117	19.5	147	10	US-09-876-997-254	Sequence 254, App
45	114.5	19.1	124	9	US-09-981-286A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-09-948-391A-24
; Sequence 24, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution
; OTHER INFORMATION: (recombinant RacoR1 Q1S)
US-09-948-391A-24

Query Match 100.0%; Score 601; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNWATFQKHINTPICNTIMDNNTIYVGQCKRVNTFISSATTVKALCTGVNNVL 60
|||||

Db 82 VLSTIRFQLNTCTTSITPRCPYSSRTENNIVICVKCENQYVHFAGIGRC 132
 RESULT 8
 Q98SL9 PRELIMINARY; PRT; 133 AA.
 ID AC Q98SL9
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RNase A-type ribonuclease rc212 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38 (2001).
 DR EMBL; AF351210; AAK30256.1; -.
 DR HSSP; P11916; 1BC4.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRODOM; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 DR Signal.
 FT SIGNAL
 FT SIGNAL 1 22 POTENTIAL.
 SQ SEQUENCE 133 AA; 14615 MW; C8785B5236B26E54E CRC64;
 Query Match 49.5%; Score 286; DB 13; Length 133;
 Best Local Similarity 47.7%; Pred. No. 2.6e-25;
 Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;
 QY 1 QDWLTFOKKHLTNRDVCNNKSTNLF---HCKDKNTFTYSPPEVKAICKGIIASKN 56
 Db 23 QNWATFOKKHITNTSSINCNNMNSLIYVGGQCKKVTIASSATTVKGICSG-VTDKK 81
 QY 57 VLTTSFYLSDCN---VTSRCKYKLKKSTNTFCVTCENQAPVHFGVGHG 104
 Db 82 VLSSTKFQLDICTRIFTPRCPYSSRTENNIVICVKCENQYVHFAGIGQC 132
 RESULT 9
 Q98SM2 PRELIMINARY; PRT; 132 AA.
 ID AC Q98SM2
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38 (2001).
 DR EMBL; AF351210; AAK30256.1; -.
 DR HSSP; P11916; 1BC4.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRODOM; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 DR Signal.
 FT SIGNAL
 FT SIGNAL 1 22 POTENTIAL.
 SQ SEQUENCE 132 AA; 14615 MW; C8785B5236B26E54E CRC64;
 Query Match 49.5%; Score 286; DB 13; Length 133;
 Best Local Similarity 47.7%; Pred. No. 2.6e-25;
 Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;
 QY 1 QDWLTFOKKHLTNRDVCNNKSTNLF---HCKDKNTFTYSPPEVKAICKGIIASKN 56
 Db 23 QNWATFOKKHITNTSSINCNNMNSLIYVGGQCKKVTIASSATTVKGICSG-VTDKK 81
 QY 57 VLTTSFYLSDCN---VTSRCKYKLKKSTNTFCVTCENQAPVHFGVGHG 104
 Db 82 VLSSTKFQLDICTRIFTPRCPYSSRTENNIVICVKCENQYVHFAGIGQC 132
 RESULT 9
 Q98SM2 PRELIMINARY; PRT; 132 AA.
 ID AC Q98SM2
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38 (2001).
 DR EMBL; AF351210; AAK30256.1; -.
 DR HSSP; P11916; 1BC4.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRODOM; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 DR Signal.
 FT SIGNAL
 FT SIGNAL 1 22 POTENTIAL.
 SQ SEQUENCE 132 AA; 14615 MW; C8785B5236B26E54E CRC64;
 Query Match 49.5%; Score 286; DB 13; Length 133;
 Best Local Similarity 47.7%; Pred. No. 2.6e-25;
 Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;
 QY 1 QDWLTFOKKHLTNRDVCNNKSTNLF---HCKDKNTFTYSPPEVKAICKGIIASKN 56
 Db 23 QNWATFOKKHITNTSSINCNNMNSLIYVGGQCKKVTIASSATTVKGICSG-VTDKK 81
 QY 57 VLTTSFYLSDCN---VTSRCKYKLKKSTNTFCVTCENQAPVHFGVGHG 104
 Db 82 VLSSTKFQLDICTRIFTPRCPYSSRTENNIVICVKCENQYVHFAGIGQC 132
 RESULT 9
 Q98SM2 PRELIMINARY; PRT; 132 AA.
 ID AC Q98SM2
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38 (2001).
 DR EMBL; AF351210; AAK30256.1; -.
 DR HSSP; P11916; 1BC4.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRODOM; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 DR Signal.
 FT SIGNAL
 FT SIGNAL 1 22 POTENTIAL.
 SQ SEQUENCE 132 AA; 14615 MW; C8785B5236B26E54E CRC64;
 Query Match 49.5%; Score 286; DB 13; Length 133;
 Best Local Similarity 47.7%; Pred. No. 2.6e-25;
 Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;
 QY 1 QDWLTFOKKHLTNRDVCNNKSTNLF---HCKDKNTFTYSPPEVKAICKGIIASKN 56
 Db 23 QNWATFOKKHITNTSSINCNNMNSLIYVGGQCKKVTIASSATTVKGICSG-VTDKK 81
 QY 57 VLTTSFYLSDCN---VTSRCKYKLKKSTNTFCVTCENQAPVHFGVGHG 104
 Db 82 VLSSTKFQLDICTRIFTPRCPYSSRTENNIVICVKCENQYVHFAGIGQC 132
 RESULT 9
 Q98SM2 PRELIMINARY; PRT; 132 AA.
 ID AC Q98SM2
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

```
Db 24 QNWETFQKKHLTDRDVKDAEMKALFDCKQNTFIYARPGVQALCKNIIVSKNVLST 83
QY 61 SEFYSDCNVTSRPPCKYKLGKSTNTFCVTNCNQAPVHFVGVGHC 104
Db 84 DEFYLSDCNRKLPCHYKLGKSSNTICITCENKLPVHFVAVBEC 127

RESULT 5
Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; 10NC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT CHAIN 24 128 RC-RNase3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.8%; Score 311; DB 13; Length 128;
Best Local Similarity 54.8%; Pred. No. 3.2e-28;
Matches 57; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTT 60
Db 24 QDWETFQKKHLTDRDVKDAEMKALFDCKQNTFIYALPGRVKALCKNIIRDNDVLSR 83

QY 61 SEFYSDCNVTSRPPCKYKLGKSTNTFCVTNCNQAPVHFVGVGHC 104
Db 84 DAFLLPQCDRIKLPCHYKLGKSSNTICITCUNQLPIHFAGVGC 127

RESULT 6
Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242556; AAG31442.2; -.
DR HSSP; P22069; 10NC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT CHAIN 24 128 RC-RNase6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.8%; Score 311; DB 13; Length 128;
Best Local Similarity 54.8%; Pred. No. 3.2e-28;
Matches 57; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTT 60
Db 24 QDWETFQKKHLTDRDVKDAEMKALFDCKQNTFIYALPGRVKALCKNIIRDNDVLSR 83

QY 61 SEFYSDCNVTSRPPCKYKLGKSTNTFCVTNCNQAPVHFVGVGHC 104
Db 84 DAFLLPQCDRIKLPCHYKLGKSSNTICITCUNQLPIHFAGVGC 127

RESULT 7
Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF31209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 51.6%; Score 298; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 1.1e-26;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKN 56
Db 23 QNWAIFQQRHINTSSINCNTMDNNIYVGGQCKGWNFISSATTVKALCTGVI-NMN 81
QY 57 VLTTFSEFYSDC--NVTSPCKYKLGKSTNTFCVTNCNQAPVHFVGVGHC 104
```

```
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242556; AAG31442.2; -.
DR HSSP; P22069; 10NC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFBFD67D266C7C2 CRC64;

Query Match 53.5%; Score 309; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 5.4e-28;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTT 60
Db 24 QDWDTFQKKHLTDRDVKDAEMKALFDCKQNTFIYARPPRVQALCKNIKNTNLSR 83

QY 61 SEFYSDCNVTSRPPCKYKLGKSTNTFCVTNCNQAPVHFVGVGHC 104
Db 84 DVFYLPQCDRIKLPCHYKLGKSSNTICITCMLKELFIHFAGVGC 127

RESULT 7
Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF31209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 51.6%; Score 298; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 1.1e-26;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKN 56
Db 23 QNWAIFQQRHINTSSINCNTMDNNIYVGGQCKGWNFISSATTVKALCTGVI-NMN 81
QY 57 VLTTFSEFYSDC--NVTSPCKYKLGKSTNTFCVTNCNQAPVHFVGVGHC 104
```

```

Db 24 QDWLTFQKKHLTNTDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
QY 61 SEFYLSDCNVTSRPCKYKLYKKSNTFCVTCENQAPVHFVGVGHC 104
Db 84 SEFYLSDCNVTSRPCKYKLYKKSNTFCVTCENQAPVHFVGVGHC 127

RESULT 2
Q8UVX5
ID Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RL "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match 96.2%; Score 556; DB 13; Length 127;
Best Local Similarity 96.2%; Pred. No. 1.2e-56;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLTNTDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Db 24 QDWLTFQKKHLTNTDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
QY 61 SEFYLSDCNVTSRPCKYKLYKKSNTFCVTCENQAPVHFVGVGHC 104
Db 84 SEFYLSDCNVTSRPCKYKLYKKSNTFCVTCENQAPVHFVGVGHC 127

RESULT 3
Q9DFY6
ID Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RX MEDLINE=20512555; PubMed=11058105;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 66.8%; Score 386; DB 13; Length 128;
Best Local Similarity 67.3%; Pred. No. 6.4e-37;
Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLTNTDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60

```

```

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31441.2; -.
DR PDB; 1KVZ; 28-JUL-02.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 70.0%; Score 404.5; DB 13; Length 129;
Best Local Similarity 67.6%; Pred. No. 4.6e-39;
Matches 71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 1 QDWLTFQKKHLTNTDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Db 24 QDWLTFQKKHLTNTDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
QY 61 SEFYLSDCNVTSRPCKYKLYKKSNTFCVTCENQAPVHFVGVGHC 104
Db 84 SEFYLAECNVKPKCKYKLYKKSNTFCVTCENQAPVHFVGVGHC 128

RESULT 4
Q9DFY8
ID Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 66.8%; Score 386; DB 13; Length 128;
Best Local Similarity 67.3%; Pred. No. 6.4e-37;
Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLTNTDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.5753 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-2
Perfect score: 578
Sequence: 1 QDLWTFQKKHLNTRDVCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	578	100.0	127	13	Q918V8	Q918v8 rana pipien
2	556	96.2	127	13	Q8UVX5	Q8uvx5 rana pipien
3	404.5	70.0	129	13	Q9DFY6	Q9dfy6 rana catesb
4	386	66.8	128	13	Q9DFY8	Q9dfy8 rana catesb
5	311	53.8	128	13	Q9DFY7	Q9dfy7 rana catesb
6	309	53.5	128	13	Q9DFY5	Q9dfy5 rana catesb
7	298	51.6	133	13	Q98SM0	Q98sm0 rana catesb
8	286	49.5	133	13	Q98SL9	Q98sl9 rana catesb
9	285	49.3	132	13	Q98SM2	Q98sm2 rana catesb
10	282	48.8	133	13	Q98SL8	Q98sl8 rana catesb
11	280	48.4	132	13	Q98SM1	Q98sm1 rana catesb
12	275.5	47.7	132	13	Q9DF78	Q9df78 rana catesb
13	157.5	27.2	169	13	Q9W738	Q9w738 xenopus lae
14	129.5	22.4	146	6	Q861Y3	Q861y3 pygathrix r
15	129.5	22.4	146	6	Q861Y2	Q861y2 pygathrix b
16	129.5	22.4	146	6	Q861Y1	Q861y1 pygathrix a

17	129	22.3	152	11	Q9JK15	Q9jk15 mus saxicol
18	127	22.0	157	11	Q9JK19	Q9jk19 meriones un
19	126.5	21.9	153	11	Q9JK17	Q9jk17 mus saxicol
20	126	21.8	157	11	Q9JK73	Q9jk73 meriones un
21	125.5	21.7	146	6	Q861Y4	Q861y4 trachypithe
22	125	21.6	157	11	Q9JKJ4	Q9jkj4 meriones un
23	123	21.3	154	11	Q9JK18	Q9jk18 mus saxicol
24	122	21.1	157	11	Q9JKJ1	Q9jkj1 meriones un
25	121	20.9	147	6	Q7YRJ6	Q7yrj6 balaena mys
26	121	20.9	157	11	Q9JKJ2	Q9jkj2 meriones un
27	120.5	20.8	155	11	Q9JKH9	Q9jkh9 mus pahari
28	119.5	20.7	155	11	Q9JKI3	Q9jki3 mus saxicol
29	118	20.4	147	6	Q7YRJ5	Q7yrj5 tursiops tr
30	116.5	20.2	155	11	Q9JKI6	Q9jk16 mus saxicol
31	115.5	20.0	132	6	Q9TV25	Q9tv25 eulemur ful
32	115.5	20.0	155	11	Q9JKI2	Q9jk12 mus saxicol
33	115.5	20.0	155	11	Q9JKI4	Q9jki4 mus saxicol
34	115	19.9	146	6	Q861Y5	Q861y5 colobus que
35	114.5	19.8	170	6	Q9BEC1	Q9bec1 tragulus ja
36	113.5	19.6	119	6	Q9TSQ6	Q9tsq6 cercopithec
37	113.5	19.6	119	6	Q9TV32	Q9tv32 gorilla gor
38	113.5	19.6	132	6	Q9TV24	Q9tv24 galago moho
39	113.5	19.6	147	6	Q8HZQ0	Q8hzq0 pan troglod
40	113.5	19.6	155	11	Q9R134	Q9r134 rattus norv
41	113	19.6	156	11	Q9JKG6	Q9jkg6 mus caroli
42	113	19.6	156	11	Q9JKH7	Q9jkh7 mus caroli
43	112.5	19.5	119	6	Q9TV30	Q9tv30 saguinus oe
44	112.5	19.5	155	11	Q9R125	Q9r125 mus musculu
45	112.5	19.5	155	11	Q9JKH8	Q9jkh8 mus pahari

ALIGNMENTS

RESULT 1

Q918V8
ID Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE Onconase variant rap1L1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure."
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165113; AAF76935.1; -
DR PIR; A39035; A39035.
DR HSSP; P22069; 10NC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00032; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 100.0%; Score 578; DB 13; Length 127;

Best Local Similarity 100.0%; Pred.No. 3.5e-59;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDLWTFQKKHLNTRDVCNIMSTNLFCHKDKNTFIYSPFPVKAICGIIASKNVLT 60

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 and GlnSer
; OTHER INFORMATION: substitution (recombinant Met(-1) RnPLR1 Q1S)
US-09-348-391A-13

Query Match
Best Local Similarity 47.1%; Score 285.5; DB 10; Length 105;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 34;

Qy 1 MSNWATFOQKHINT-PIICNTIMDNNIYIVGGQCKRVNTFIISATTVKAICTGVI -NM 58
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MSDWLIFQKHLINTRVDCNNIMSTNLF---HCKDKNTFIYSRPFVKAI CKGIASK 56
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 59 NVLSTTRFQALNCTRTSITPRCPYSSRTFTNYICVKENQYVPHFAGIGRC 110
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 57 NVLTTSFIFYLSDC---NVTGRPKYKLLKSTNTPFCVTCEQAQPVHFFVGVGHC 105
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: May 11, 2004, 14:39:23
Job time : 38.1719 secs

GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
CELLS
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 09/622,613
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 117
TYPE: PRT
ORGANISM: Rana catesbeiana
US-09-961-400-22

Query Match 98.3%; Score 596; DB 10; Length 117;
Best Local Similarity 97.3%; Pred. No. 7e-60;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKATCTGVINNV 60
DB 7 MGNATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKATCTGVINNV 66

QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 67 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 13
US-09-961-400-19
Sequence 19, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 09/622,613
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 110
TYPE: PRT
ORGANISM: Rana catesbeiana
US-09-961-400-19

Query Match 97.5%; Score 591; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 2.4e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKATCTGVINNV 62
DB 2 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKATCTGVINNV 61

QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
|||||

DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
RESULT 14
US-09-948-391A-19
Sequence 19, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: NEWTON, DIANNE L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rana
catesbeiana ribonuclease with Met22Leu and
OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1
Met57Leu)

US-09-948-391A-19

Query Match 96.5%; Score 585; DB 10; Length 110;
Best Local Similarity 97.2%; Pred. No. 1.2e-58;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKATCTGVINNV 62
DB 2 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKATCTGVINNV 61

QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 15
US-09-948-391A-13
Sequence 13, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: NEWTON, DIANNE L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 105

RESULT 10
US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26

```
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-24

Query Match
Best Local Similarity 99.2%; Score 601; DB 10; Length 110;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
DB 1 SNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 60
QY 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 6
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match
Best Local Similarity 98.5%; Score 597; DB 10; Length 110;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 62
DB 2 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 7
US-09-961-400-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match
Best Local Similarity 100.0%; Pred. No. 5e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 62
DB 2 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 7
US-09-961-400-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match
Best Local Similarity 100.0%; Pred. No. 5e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 62
DB 2 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 7
US-09-961-400-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match
Best Local Similarity 98.3%; Score 596; DB 10; Length 111;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-15

Query Match
Best Local Similarity 100.0%; Pred. No. 5e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 62
DB 2 NWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 8
US-09-948-391A-17
; Sequence 17, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: (recombinant Met(-1) RaCOR1)
US-09-948-391A-17

Query Match
Best Local Similarity 98.2%; Score 596; DB 10; Length 111;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```


Db 1 MSNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKACTGVINNV 60
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2

US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

Query Match 100.0%; Score 606; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.8e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKACTGVINNV 60
Db 1 MSNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKACTGVINNV 60
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3

US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-17

Query Match 99.3%; Score 602; DB 10; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.4e-60;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKACTGVINNV 60
Db 1 MSNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKACTGVINNV 60
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 4

US-09-948-391A-24
; Sequence 24, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Gln>Ser substitution
; OTHER INFORMATION: (recombinant RacOR1 Q1S)
US-09-948-391A-24

Query Match 99.2%; Score 601; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKACTGVINNV 61
Db 1 SNWATFQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKACTGVINNV 60
QY 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 5

US-09-961-400-24
; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:34:38 ; Search time 38.1719 Seconds
(without alignments)
807.135 Million cell updates/sec

Title: US-09-961-400-26

Perfect score: 606

Sequence: 1 MSNWATFQKHINTPIIGN.....ICVKENQYVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	606	100.0	111	10	US-09-948-391A-26
2	606	100.0	111	10	US-09-961-400-26
3	602	99.3	111	10	US-09-961-400-17
4	601	99.2	110	10	US-09-948-391A-24
5	601	99.2	110	10	US-09-961-400-24
6	597	98.5	110	10	US-09-948-391A-15
7	597	98.5	110	10	US-09-961-400-15
8	596	98.3	111	10	US-09-948-391A-17
9	596	98.3	111	10	US-09-948-391A-21
10	596	98.3	111	10	US-09-961-400-21
11	596	98.3	117	10	US-09-948-391A-22
12	596	98.3	117	10	US-09-961-400-22
13	591	97.5	110	10	US-09-961-400-19
14	585	96.5	110	10	US-09-948-391A-19
15	285.5	47.1	105	10	US-09-948-391A-13

16	285.5	47.1	105	10	US-09-961-400-13	Sequence 13, Appl
17	281.5	46.5	105	10	US-09-948-391A-6	Sequence 6, Appli
18	281.5	46.5	105	10	US-09-961-400-6	Sequence 6, Appli
19	280.5	46.3	104	10	US-09-948-391A-11	Sequence 11, Appl
20	280.5	46.3	104	10	US-09-961-400-11	Sequence 11, Appl
21	278.5	46.0	111	10	US-09-961-400-9	Sequence 9, Appli
22	277.5	45.8	105	14	US-10-153-882-2	Sequence 2, Appli
23	276.5	45.6	104	10	US-09-961-400-2	Sequence 2, Appli
24	276.5	45.6	127	10	US-09-948-391A-28	Sequence 28, Appl
25	276.5	45.6	127	10	US-09-961-400-28	Sequence 28, Appl
26	275.5	45.5	104	10	US-09-948-391A-2	Sequence 2, Appli
27	275.5	45.5	105	10	US-09-961-400-8	Sequence 8, Appli
28	272.5	45.0	104	9	US-09-986-119-1	Sequence 1, Appli
29	272.5	45.0	104	10	US-09-918-887-1	Sequence 1, Appli
30	270.5	44.6	104	10	US-09-948-391A-4	Sequence 4, Appli
31	270.5	44.6	104	10	US-09-961-400-4	Sequence 4, Appli
32	266.5	44.0	105	10	US-09-948-391A-8	Sequence 8, Appli
33	266.5	44.0	111	10	US-09-948-391A-9	Sequence 9, Appli
34	264.5	43.6	104	12	US-10-461-713-53	Sequence 53, Appl
35	206	34.0	83	9	US-09-986-119-3	Sequence 3, Appli
36	206	34.0	83	10	US-09-918-887-3	Sequence 3, Appli
37	158	26.1	169	13	US-10-016-447-2	Sequence 2, Appli
38	135.5	22.4	124	12	US-10-037-417-103	Sequence 103, App
39	126.5	20.9	119	12	US-10-016-248-89	Sequence 89, Appl
40	126.5	20.9	119	15	US-10-074-978A-139	Sequence 139, App
41	121	20.0	99	15	US-10-074-978A-141	Sequence 141, App
42	117.5	19.4	124	12	US-10-461-713-52	Sequence 52, Appl
43	117	19.3	147	9	US-09-731-872-254	Sequence 254, App
44	117	19.3	147	10	US-09-876-997-254	Sequence 254, App
45	114.5	18.9	124	9	US-09-981-286A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RacOR1 Q1S)
US-09-948-391A-26

Query Match 100.0%; Score 606; DB 10; Length 111;
Best Local Similarity 100.0%; Pred No. 4.8e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSNWATFQKHINTPIIGNNTIMNNIYVGGCKRVNTFISSATTVKATGVINMV 60
|||||

Search completed: May 7, 2004, 21:46:05
Job time : 32.5659 secs

RESULT 11

Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (bullfrog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
DR EMBL; AF242554; AAG31440.2; -;
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 36.9%; Score 223.5; DB 13; Length 128;
Best Local Similarity 40.2%; Pred. No. 7.5e-18;

Matches 45; Conservative 19; Mismatches 39; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTILDNNIYVGQCKRVNTFISSATTVAICTGV-INLN 59
DB 24 QWDTFQKKHLTDTKKVKCDVEMKALF----DCKKNTTFIPAREPRVQALCKNIKDNIN 79
QY 60 VLSITRFQNTCTRTSITPRPCPYSSRTETNYICVKENQYVHPFAGIGRCP 111
DB 80 VLSRDAFLPQCDRIKL---PCHYKLSSTNTICITCVNQLPIHFAGVGSCTP 128

RESULT 12

Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (bullfrog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
DR EMBL; AF242556; AAG31442.2; -;
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 36.9%; Score 223.5; DB 13; Length 128;
Best Local Similarity 40.2%; Pred. No. 7.5e-18;

Matches 45; Conservative 19; Mismatches 39; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTILDNNIYVGQCKRVNTFISSATTVAICTGV-INLN 59
DB 24 QWDTFQKKHLTDTKKVKCDVEMKALF----DCKKNTTFIPALPRVKALCKNRDND 79
QY 60 VLSITRFQNTCTRTSITPRPCPYSSRTETNYICVKENQYVHPFAGIGRCP 111
DB 80 VLSRDAFLPQCDRIKL---PCHYKLSSTNTICITCVNQLPIHFAGVGSCTP 128

DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFE6FD67D266C7C2 CRC64;
Query Match 35.5%; Score 214.5; DB 13; Length 128;
Best Local Similarity 38.4%; Pred. No. 8.2e-17;
Matches 43; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTILDNNIYVGQCKRVNTFISSATTVAICTGV-INLN 59
DB 24 QWDTFQKKHLTDTKKVKCDVEMKALF----DCKKNTTFIPAREPRVQALCKNIKDNIN 79
QY 60 VLSITRFQNTCTRTSITPRPCPYSSRTETNYICVKENQYVHPFAGIGRCP 111
DB 80 VLSRDFVFLPQCNKKL---PCHYRLDGSSTNTICITCKMKELPIHFAGVGSCTP 128

RESULT 13

Q9W738 PRELIMINARY; PRT; 169 AA.
AC Q9W738;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE FRL2 protein.
GN FRL2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96069863; PubMed=7585965;
RA Kinoshita N., Minshull J., Kirschner M.W.;
RT "The identification of two novel ligands of the FGF receptor by a
yeast screening method and their activity in Xenopus development.";
RL Cell 83:621-630 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Kinoshita N., Kirschner M.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159166; AAD41901.1; -;
DR HSSP; P00856; ILSQ.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 169 AA; 18891 MW; D969F3E4B3CE1B8 CRC64;

Query Match 26.6%; Score 161; DB 13; Length 169;
Best Local Similarity 39.3%; Pred. No. 1.6e-10;
Matches 44; Conservative 10; Mismatches 50; Indels 8; Gaps 6;

QY 2 QNWATFOQKHII--NTPICN-TILDNNIYVGQCKRVNTFI-ISSATTVAICTGVIN 57
DB 28 QNINAFMEKHIVKEGAETNCQTIKDRNIRF--KNNCKFRNTFIHDTNGKKKEMCAGIYK 86
QY 58 LN-VLSITRFQNTCTRTSITPRP--CPYSSRTETNYICVKENQYVHPFAG 106
DB 87 STFVISKELLPLTDCLLMGRTPARPNCAYNQTRTTGVINITCENNYVHPFAG 138

RESULT 14

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

```

RESULT 5
Q98SM1
ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
EA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
KW SIGNAL.
FT SIGNAL
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 73.5%; Score 444.5; DB 13; Length 132;
Best Local Similarity 77.3%; Pred. No. 3e-43;
Matches 85; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

QY 2 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
Db 23 QDWTFQCKHPTSSSIDCNTIMDKAIYVGGQCKKNTFIYATTVKAICTGVNSNV 82

QY 61 LSTTRFQINTCTRTSITPRPCYSRTETNYICVKENQYVPHFAGIGRC 110
Db 83 LSTTRFQIXXTFTITSRPCYSSTKETNKCICVKECNEYVPHFAGIGKC 132

RESULT 6
Q9DF78
ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNaseL ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AF288642; AAG30414.2; -.

```

```

DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
KW SIGNAL.
FT CHAIN
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452PBE53 CRC64;

Query Match 61.5%; Score 372; DB 13; Length 132;
Best Local Similarity 64.9%; Pred. No. 6.5e-35;
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;

QY 2 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59
Db 22 QNWAFKEKHITSIDCNTIMDKAIYVGGQCKERNFTFISSDNVKAICSGVSPDRK 81

QY 60 VLSTTRFQINTCTRTSITPRPCYSRTETNYICVKENQYVPHFAGIGRC 110
Db 82 ELSTTSFKLNTCIRDSITPRPCYPHSPDNNKICVKCEKQLPVHFVGIGKC 132

RESULT 7
Q918V8
ID Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rapRL precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR PIR; A39035; A39035.
DR HSSP; P22069; 1ONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
KW SIGNAL.
FT SIGNAL
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 45.9%; Score 277.5; DB 13; Length 127;
Best Local Similarity 48.6%; Pred. No. 4.6e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59
Db 24 QDWLTFQCKHLNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 79

QY 60 VLSTTRFQINTCTRTSITPRPCYSRTETNYICVKENQYVPHFAGIGRC 110
Db 80 VLTTSEFYLSDC---NVTSRPCKYKLLKSTNTFCVTNCENQAPVHFVGIGHC 127

```

```

QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 111
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL J. Mol. Evol. 53:31-38(2001).";
DB 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 133

RESULT 2
Q98SM2 PRELIMINARY; PRT; 132 AA.
AC Q98SM2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL J. Mol. Evol. 53:31-38(2001).";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF351207; AAK30253.1; -.
DR EMBL; AF359578; AAL87036.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL J. Mol. Evol. 53:31-38(2001).";
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL J. Mol. Evol. 53:31-38(2001).";
DB 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 111
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL J. Mol. Evol. 53:31-38(2001).";
DB 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 133

RESULT 2
Q98SL9 PRELIMINARY; PRT; 133 AA.
AC Q98SL9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc212 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL J. Mol. Evol. 53:31-38(2001).";
DB 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 110
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL J. Mol. Evol. 53:31-38(2001).";
DB 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 132

RESULT 3
Q98SL9 PRELIMINARY; PRT; 133 AA.
AC Q98SL9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc212 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL J. Mol. Evol. 53:31-38(2001).";
DB 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 111
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL J. Mol. Evol. 53:31-38(2001).";
DB 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 133

Query Match 79.9%; Score 483.5; DB 13; Length 132;
Best Local Similarity 82.7%; Pred. No. 9.7e-48;
Matches 91; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 2 QNWATFQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLV 60
DB 23 QWATFQKHINTSSINCNSIMNNSLVVGGQCKVNTFIASSATTVKIGCSGVTDKV 82

QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 111
DB 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 133

Query Match 77.3%; Score 467.5; DB 13; Length 133;
Best Local Similarity 75.7%; Pred. No. 6.7e-46;
Matches 84; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

QY 2 QNWATFQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLV 60
DB 23 QWATFQKHINTSSINCNSIMNNSLVVGGQCKVNTFIASSATTVKIGCSGVTDKV 82

QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 111
DB 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYPVHFAGIGRCP 133

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 31.566 Seconds

(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-21

Perfect score: 605

Sequence: 1 MNWATFOQKHINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertibrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	554.5	91.7	133	13	Q98SM0 rana catesb
2	483.5	79.9	132	13	Q98SM2 rana catesb
3	474.5	78.4	133	13	Q98SL9 rana catesb
4	467.5	77.3	133	13	Q98SL8 rana catesb
5	444.5	73.5	132	13	Q98SM1 rana catesb
6	372	61.5	132	13	Q98DF78 rana catesb
7	277.5	45.9	127	13	Q918V8 rana pipien
8	273.5	45.2	127	13	Q98VX5 rana pipien
9	243	40.2	129	13	Q9DFY6 rana catesb
10	225.5	37.3	128	13	Q9DFY8 rana catesb
11	223.5	36.9	128	13	Q9DFY7 rana catesb
12	214.5	35.5	128	13	Q9DFY5 rana catesb
13	161	26.6	169	13	Q9W738 xenopus lae
14	128	21.2	170	6	Q98EC1
15	127.5	21.1	144	11	Q80Z85 mus musculus
16	127.5	21.1	153	11	Q80XS4 mus musculus

17	123.5	20.4	147	6	Q7YRJ6	Q7YRJ6 balaena mys
18	122	20.2	146	6	Q861Y5	Q861Y5 colobus gue
19	121.5	20.1	116	6	Q9TVC0	Q9TVC0 sus scrofa
20	121.5	20.1	163	6	Q9BDC2	Q9BDC2 antilocapra
21	121	20.0	150	11	Q8VD94	Q8VD94 berylmys bo
22	119	19.7	150	11	Q8VD88	Q8VD88 rattus norv
23	118.5	19.6	144	6	Q9BH14	Q9BH14 antilocapra
24	118.5	19.6	147	6	Q7YRJ5	Q7YRJ5 tursiops tr
25	116.5	19.3	149	11	Q8K2T2	Q8K2T2 mus musculus
26	116.5	19.3	149	11	Q8C6G3	Q8C6G3 mus musculus
27	116	19.2	146	6	Q861Y4	Q861Y4 trachypithe
28	115	19.2	150	11	Q8VD92	Q8VD92 rattus exul
29	115	19.0	146	6	Q861Y3	Q861Y3 pygathrix r
30	115	19.0	146	6	Q861Y2	Q861Y2 pygathrix b
31	115	19.0	146	6	Q861Y1	Q861Y1 pygathrix a
32	113.5	18.8	152	11	Q8VD89	Q8VD89 rattus norv
33	111	18.3	148	11	Q8C663	Q8C663 mus musculus
34	110.5	18.3	124	6	Q95NE6	Q95NE6 bubalus bub
35	109.5	18.1	148	11	Q8C7E4	Q8C7E4 mus musculus
36	109.5	18.1	149	11	Q8VD95	Q8VD95 berylmys bo
37	109	18.0	124	6	Q9BEC2	Q9BEC2 tragulus ja
38	109	18.0	134	6	Q9BDB9	Q9BDB9 tragulus ja
39	108.5	17.9	152	11	Q8VD84	Q8VD84 rattus tiom
40	108.5	17.9	156	6	Q8SQ05	Q8SQ05 lagothrix l
41	107.5	17.8	119	6	Q9TV28	Q9TV28 eulemur ful
42	107.5	17.8	119	6	Q9TV30	Q9TV30 saguinus oe
43	106.5	17.6	156	6	Q8SQ06	Q8SQ06 ateles geof
44	105.5	17.4	142	6	Q9BEC3	Q9BEC3 tragulus ja
45	105.5	17.4	156	6	Q8SQ08	Q8SQ08 salmiri sci

ALIGNMENTS

RESULT 1

Q98SM0

ID Q98SM0 PRELIMINARY; PRT; 133 AA.

AC Q98SM0;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE RNase A-type ribonuclease rc208 precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

ON NCBI_TaxID=8400;

RX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

bullfrog, Rana catesbeiana.";

RL J. Mol. Evol. 53:31-38(2001).

DR EMBL; AF351209; AAK30255.1; --

DR HSSP; P11916; 1BC4.

DR GO; GO:0003676; R:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; rnasea; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase PG; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

KW Signal.

FT SIGNAL.

SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match

Best Local Similarity 91.7%; Score 554.5; DB 13; Length 133;

Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 2 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFFIISATTVKAICTGVINLV 60

|||||

DB 23 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFFIISATTVKAICTGVINLV 82

Q9BEC1 Q9BEC1 PRELIMINARY; PRT; 170 AA.
AC Q9BEC1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Brain-type ribonuclease ribonuclease precursor (Fragment).
GN RNase B.
OS Tragus javanicus (Lesser Malay chevron).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
OC Tragulidae; Tragulus.
OX NCBI_TaxID=9849;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347458; PubMed=11453981;
RA Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,
RA Warmels H.W., Beintema J.J.;
RT "Secretory ribonucleases in the primitive ruminant chevrotain
RT (Tragus javanicus).";
RL Eur. J. Biochem. 268:3890-3897(2001).
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR EMBL; AJ271299; CAC24723.1; -.
DR HSSP; P00656; 1LSQ.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Endonuclease; Hydrolase; Nuclease; Signal.
FT NON TER 1
FT SIGNAL <1 19
FT CHAIN 20 170
FT SEQUENCE 170 AA; 18832 MW; AB6CE7E1E5549AA0 CRC64;
Query Match 21.6%; Score 131; DB 6; Length 170;
Best Local Similarity 33.1%; Pred. No. 2.8e-07;
Matches 41; Conservative 17; Mismatches 46; Indels 20; Gaps 7;

QY 5 ATFOCKH-----INTPIICNTIMNNIYVGGCKRVNTFISSATTVKAICT----- 53
DB 25 AKFRQHLDAAGNSINSN-YCNLMKKR-KMTHGRCKPVNTFTHESLEDVKAICSEKNIT 82
QY 54 ---GVINMNVLTFRFQINTCTRTSITRP-CPYSSRTETNYICVKCN--QYPVHPAGI 107
DB 83 CKGQPNCHQSNST-MNITDCRTGSGKYPNCAYKTSQKQYIIVACEGTPSPVHPFDGS 141
QY 108 GRCP 111
DB 142 AVLP 145

RESULT 15
Q80285 Q80285 PRELIMINARY; PRT; 144 AA.
AC Q80285;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Angiogenin-4.
GN ANG4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NMRI;
MEDLINE=22493143; PubMed=12548285;

RA Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I.;
RT "Angiogenins: a new class of microbicidal proteins involved in innate
RT immunity.";
RL Nat. Immunol. 4:269-273(2003).
DR EMBL; AY219870; AAO62354.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 144 AA; 16554 MW; 09808807C00224C1 CRC64;
Query Match 21.2%; Score 128.5; DB 11; Length 144;
Best Local Similarity 38.2%; Pred. No. 4.6e-07;
Matches 29; Conservative 13; Mismatches 29; Indels 5; Gaps 3;

QY 34 CKRVNTFISSATTVKAIC---TGVINMNV-LSTTRFQINTCTRTSITP-RPCPYSSRTE 88
DB 62 CKDWNTHGTTKKNIRAIKCKGSGPYGENFRISNPFQITCTHRSRGPWPVPCGAFKD 121
QY 89 TNYICVKCNQYPVHF 104
DB 122 FRYIVACEDGWPVHF 137
Search completed: May 11, 2004, 14:36:30
Job time : 36.6606 secs

RESULT 11
 Q9DFY7 Q9DFY7 PRELIMINARY; PRT; 128 AA.
 AC Q9DFY7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RC-RNase3 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 DR EMBL; AF242554; AAC31440.2; -;
 DR HSP; P22069; IONC.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 PFam; PF00074; rnaseaA; 1.
 ProDom; PD000535; RNaseA; 1.
 PROSITE; PS00127; RNASE_PANCREATIC; 1.
 FT SIGNAL.
 KW SIGNAL.
 FT CHAIN 1 23 POTENTIAL.
 FT CHAIN 24 128 RC-RNase3 RIBONUCLEASE.
 SQ SEQUENCE 128 AA; 14517 MW; 2814986082R0587D CRC64;
 Query Match 36.6%; Score 221.5; DB 13; Length 128;
 Best Local Similarity 40.5%; Pred. No. 5.7e-18;
 Matches 45; Conservative 18; Mismatches 39; Indels 9; Gaps 4;
 Qy 3 NWATFOQKHII-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGV-INNV 60
 Db 25 DWETFOKKHLTDTKVKCDVEMAKLF---DCKTNTFIYALPGRVKALCKNRDNTDV 80
 Qy 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111
 Db 81 LSRDAFLPQCDRIKL---PCHYKLSSSTNTICITCNQNLPIHFAGVGS 128
 Query Match 36.6%; Score 221.5; DB 13; Length 128;
 Best Local Similarity 40.5%; Pred. No. 5.7e-18;
 Matches 45; Conservative 18; Mismatches 39; Indels 9; Gaps 4;
 Qy 3 NWATFOQKHII-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGV-INNV 60
 Db 25 DWETFOKKHLTDTKVKCDVEMAKLF---DCKTNTFIYALPGRVKALCKNRDNTDV 80
 Qy 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111
 Db 81 LSRDAFLPQCDRIKL---PCHYKLSSSTNTICITCNQNLPIHFAGVGS 128
 RESULT 12
 Q9DFY5 Q9DFY5 PRELIMINARY; PRT; 128 AA.
 AC Q9DFY5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RC-RNase6 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 DR EMBL; AF242556; AAC31442.2; -;
 DR HSP; P22069; IONC.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 PFam; PF00074; rnaseaA; 1.
 ProDom; PD000535; RNaseA; 1.
 PROSITE; PS00127; RNASE_PANCREATIC; 1.
 FT SIGNAL.
 KW SIGNAL.
 FT CHAIN 1 23 POTENTIAL.
 FT CHAIN 24 128 RC-RNase6 RIBONUCLEASE.
 SQ SEQUENCE 128 AA; 14517 MW; 2814986082R0587D CRC64;
 Query Match 36.6%; Score 221.5; DB 13; Length 128;
 Best Local Similarity 40.5%; Pred. No. 5.7e-18;
 Matches 45; Conservative 18; Mismatches 39; Indels 9; Gaps 4;
 Qy 3 NWATFOQKHII-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGV-INNV 60
 Db 25 DWETFOKKHLTDTKVKCDVEMAKLF---DCKTNTFIYALPGRVKALCKNRDNTDV 80
 Qy 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111
 Db 81 LSRDAFLPQCDRIKL---PCHYKLSSSTNTICITCNQNLPIHFAGVGS 128

```

RESULT 8
Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RM EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CPEEF3 CRC64;

Query Match 45.0%; Score 272.5; DB 13; Length 127;
Best Local Similarity 49.1%; Pred. No. 6.3e-24;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 3 NWATFOQKHINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVI-MNNV 60
Db 25 DWLTFQKKHITDTRDVKDCNIMSTLNF---HCKDKNTFIYSRPEPVKAICKGIASKNV 80
QY 61 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 81 LTTSEFYLSDC---NVTSRPPCKYKLLKSSNTRICRHELPVHFAGVGSC 127

RESULT 9
Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RM EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.0%; Score 224.5; DB 13; Length 128;
Best Local Similarity 39.6%; Pred. No. 2.6e-18;
Matches 44; Conservative 20; Mismatches 38; Indels 9; Gaps 4;

QY 3 NWATFOQKHINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVI-MNNV 60
Db 25 NWETFQKKHITDTRDVKDCNIMSTLNF---DCKDKNTFIYSRPEPVKAICKGIASKNV 80
QY 61 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 111
Db 81 LSTDDEFYLSDCNRIKL---PCHYKLLKSSNTICITCENKLPVHFVAVEECP 128

```

```

InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 39.8%; Score 241; DB 13; Length 129;
Best Local Similarity 42.9%; Pred. No. 3.1e-20;
Matches 48; Conservative 24; Mismatches 30; Indels 10; Gaps 5;

QY 3 NWATFOQKHINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVI-MNNV 60
Db 25 DWATEKKHITDTRDVKDCNIMSTLNF---DCKDKNTFIYSRPEPVKAICKGIASKNV 80
QY 61 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 111
Db 81 LSNSEFYLAEC---NVKPRPKCKYKLLKSSNTRICRHELPVHFAGVGICP 129

RESULT 10
Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RM EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.0%; Score 224.5; DB 13; Length 128;
Best Local Similarity 39.6%; Pred. No. 2.6e-18;
Matches 44; Conservative 20; Mismatches 38; Indels 9; Gaps 4;

QY 3 NWATFOQKHINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVI-MNNV 60
Db 25 NWETFQKKHITDTRDVKDCNIMSTLNF---DCKDKNTFIYSRPEPVKAICKGIASKNV 80
QY 61 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 111
Db 81 LSTDDEFYLSDCNRIKL---PCHYKLLKSSNTICITCENKLPVHFVAVEECP 128

```

```

RESULT 5
Q98SM1
ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;
EX MEDLINE=21539506; PubMed=11583320;
RA Rosenberg H.F.; Zhang J.; Liao Y.-D.; Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38 (2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
RW Signal.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 73.2%; Score 443.5; DB 13; Length 132;
Best Local Similarity 78.0%; Pred. No. 7.3e-44;
Matches 85; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 3 NWATFOQKHINTPIL-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNV 61
DB 24 DWLTFQKHINTPSTSSIDCNTIMDKIYVGGCKRVNTFISSATTVKAICTGVINMNV 93

QY 62 STTRFQNTCTRTSITPRPCYSSTRTNYICVKCENQYPVHFAGIGRC 110
DB 84 STTRFQXXTRTFTSITPRPCYSSTRTNYICVKCENQYPVHFAGIGRC 132

RESULT 6
Q9DF78
ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D.; Huang H.-C.; Leu Y.-J.; Wei C.-W.; Tang P.-C.; Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D.; Huang H.-C.; Leu Y.-J.; Wei C.-W.; Tang P.-C.; Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286642; AAG30414.2; -.

```

```

DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 132 RC-RNASEL1 RIBONUCLEASE.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FB53 CRC64;

Query Match 61.2%; Score 371; DB 13; Length 132;
Best Local Similarity 65.5%; Pred. No. 2.1e-35;
Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 3 NWATFOQKHINTPIL-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNV 60
DB 23 NWAKFKKHITSTSSIDCNTIMDKIYVGGCKRVNTFISSATTVKAICTGVINMNV 82

QY 61 LSTTRFQNTCTRTSITPRPCYSSTRTNYICVKCENQYPVHFAGIGRC 110
DB 83 LSTTSFKLNTCTRTSITPRPCYPHPSPDNKIKCKEQLPVHFVGIGKC 132

RESULT 7
Q918V8
ID Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rap1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L.; Le S.-Y.; Newton D.L.; Maizel J.V. Jr.; Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure."
RL Nucleic Acids Res. 28:2375-2382 (2000).
DR EMBL; AF165133; AAF78935.1; -.
DR PIR; A39035; A39035.
DR HSSP; P22069; 1ONG.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT CHAIN 22 132 RC-RNASEL1 RIBONUCLEASE.
SQ SEQUENCE 127 AA; 14491 MW; B8511DCS407AB69B CRC64;

Query Match 45.6%; Score 276.5; DB 13; Length 127;
Best Local Similarity 49.1%; Pred. No. 2.2e-24;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 3 NWATFOQKHINTPIL-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNV 60
DB 25 DWLTFQKHINTTRDVCNNIMSTNLF----HCKKNTFIYSRPEPVKAICKGIIASKNV 80

QY 61 LSTTRFQNTCTRTSITPRPCYSSTRTNYICVKCENQYPVHFAGIGRC 110
DB 81 LITSEFYLSDC---NVTSPCKYKLLKKSINTFCVTCENQAPVHFVGIGHC 127

```

Db 84 SSNKFQDLICTRIFITPRPCPISSRTEINYICVKCENQYPVHFAGIGQCP 133

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:30:53 ; Search time 35.6606 Seconds

(without alignments)
982.106 Million cell updates/sec

Title: US-09-961-400-26

Perfect score: 606

Sequence: 1 MNWATFOQKHINTPLCN.....ICVKCENQYVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL, 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	555.5	91.7	133	Q98SM0	Q98sm0 rana catesb
2	482.5	79.6	132	Q98SM2	Q98sm2 rana catesb
3	463.5	78.1	133	Q98SL9	Q98sl9 rana catesb
4	466.5	77.0	133	Q98SL8	Q98sl8 rana catesb
5	443.5	73.2	132	Q98SM1	Q98sm1 rana catesb
6	371	61.2	132	Q98DF78	Q9df78 rana catesb
7	276.5	45.6	127	Q918V8	Q918v8 rana pipien
8	272.5	45.0	127	Q98UVX5	Q98uvx5 rana pipien
9	241	39.8	129	Q9DFY6	Q9dfy6 rana catesb
10	224.5	37.0	128	Q9DFY8	Q9dfy8 rana catesb
11	221.5	36.6	128	Q9DFY7	Q9dfy7 rana catesb
12	212.5	35.1	128	Q9DFY5	Q9dfy5 rana catesb
13	158	26.1	169	Q9W738	Q9w738 xenopus lae
14	131	21.6	170	Q9BEC1	Q9bec1 tragulus ja
15	128.5	21.2	144	Q80Z85	Q80z85 mus musculus
16	128.5	21.2	153	Q80XS4	Q80xs4 mus musculus

17	127.5	21.0	147	6	Q7YRJ6	Q7yrj6 balaena mys
18	126	20.8	150	11	Q8VD94	Q8vd94 berylmys bo
19	125.5	20.7	163	6	Q9BDC2	Q9bdc2 antilocapra
20	124.5	20.5	116	6	Q9TVC0	Q9tvc0 sus scrofa
21	124	20.5	150	11	Q8VD88	Q8vd88 rattus norv
22	123.5	20.4	146	6	Q861Y4	Q861y4 trachypithe
23	122.5	20.2	144	6	Q9BH14	Q9bh14 antilocapra
24	122.5	20.2	146	6	Q861Y3	Q861y3 pygathrix r
25	122.5	20.2	146	6	Q861Y2	Q861y2 pygathrix b
26	122.5	20.2	146	6	Q861Y1	Q861y1 pygathrix a
27	121.5	20.0	147	6	Q7YRJ5	Q7yrj5 tursiops tr
28	121	20.0	146	6	Q861Y5	Q861y5 colobus gue
29	120.5	19.9	149	11	Q8K2F2	Q8k2f2 mus musculu
30	120.5	19.9	149	11	Q8CG3	Q8cg3 mus musculu
31	120	19.8	150	11	Q8VD92	Q8vd92 rattus exul
32	116.5	19.2	152	11	Q8VD89	Q8vd89 rattus norv
33	114.5	18.9	124	6	Q9SNE6	Q9sne6 bubalus bub
34	112.5	18.6	148	11	Q8C7E4	Q8c7e4 mus musculu
35	112.5	18.6	149	11	Q8VD95	Q8vd95 berylmys bo
36	112	18.5	134	6	Q9BDB9	Q9bdb9 tragulus ja
37	111.5	18.4	152	11	Q8VD84	Q8vd84 rattus tiom
38	111.5	18.4	156	6	Q8SQ05	Q8sq05 lagotherix l
39	111	18.3	148	11	Q8C6E3	Q8c6e3 mus musculu
40	110.5	18.2	119	6	Q9TV28	Q9tv28 eulemur ful
41	110.5	18.2	119	6	Q9TV30	Q9tv30 saguinus oe
42	109.5	18.1	142	6	Q9BEC3	Q9bec3 tragulus ja
43	109.5	18.1	156	6	Q8SQ06	Q8sq06 ateles geof
44	109	18.0	124	6	Q9BEC2	Q9bec2 tragulus ja
45	108.5	17.9	156	6	Q8SQ08	Q8sq08 saimiri sci

ALIGNMENTS

RESULT 1

Q98SM0 PRELIMINARY; PRT; 133 AA.
ID Q98SM0; AC Q98SM0; DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38 (2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL. 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 91.7%; Score 555.5; DB 13; Length 133;

Best Local Similarity 94.5%; Pred. No. 6.3e-57;

Matches 104; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 3 NWATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFIISATTVKAICTGVINNV 61

DB 24 NWATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFIISATTVKAICTGVINNV 83

99BEC1	Q9BEC1	PRELIMINARY;	PRT;	170 AA.
Q9BEC1	Q9BEC1			
01-JUN-2001	(TREMBLrel. 17, Created)			
01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
01-JUN-2003	(TREMBLrel. 24, Last annotation update)			
Brain-type ribonuclease ribonuclease precursor (Fragment).				
RNAse B.				
Tragulus javanicus (Lesser Malay chevrotain).				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;				
Tragulidae; Tragulus.				
NCBI_TaxID=9849;				
NCBI				
SEQUENCE FROM N.A.				
MEDLINE=21347459; PubMed=11453981;				
Bruckelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,				
Waxmels H.W., Beintema J.J.;				
"Secretory ribonucleases in the primitive ruminant chevrotain				
(Tragulus javanicus)".				
Eur. J. Biochem. 268:3890-3897(2001).				
-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
EMBL; AJ271299; CAC24723.1; -.				
HSSP; P00656; ILISQ.				
GO; GO:0004519; F:endonuclease activity; IEA.				
GO; GO:0016787; F:hydrolase activity; IEA.				
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.				
InterPro; IPR001427; RNaseA.				
Pfam; PF00074; rnaseA; 1.				
PRINTS; PR00794; RIBONUCLEASE.				
ProDom; PD000535; RNaseA; 1.				
SMART; SM00092; RNase Pc; 1.				
PROSITE; PS00127; RNASE PANCREATIC; 1.				
Endonuclease; Hydrolase; Nuclease; Signal.				
NON TER 1				
SIGNAL <1				
CHAIN 20 170				
SEQUENCE 170 AA; 18832 MW; AB6CE7ELE5549AA0 CRC64;				
Query March 21.8%; Score 131; DB 6; Length 170;				
Best Local Similarity 33.1%; Pred No. 2.8e-07;				
Matches 41; Conservative 17; Mismatches 46; Indels 20; Gaps 7				
Qy	4	ATFOQKHI-----INTPIICNTIMDNMIYVGGQCKRVNTFISSATTVKAICT-----52		
Db	25	AKFRQHLDAAGNSSINSN-YCNLMKKR-KWTHGRCKPVNTFIHSLSDVKAICSEKNIT82		
Qy	53	---GVINNVLSITRRFQINICTRTSITPRP-CYSSSTETNIYCKVCEN--QYPVHFAGI106		
Db	83	CKNGOPNCHOSNST-KNITDCRQTGGSKPNCAYKTSQKQYIIVACEGTPSPVHFDS141		
Qy	107	GRCP 110		
Db	142	AVLP 145		
RESULT 15				
Q80Z85	Q80Z85	PRELIMINARY;	PRT;	144 AA.
Q80Z85	Q80Z85			
01-JUN-2003	(TREMBLrel. 24, Created)			
01-JUN-2003	(TREMBLrel. 24, Last sequence update)			
01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
Angiogenin-4.				
Mus musculus (Mouse).				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090;				
NCBI				
SEQUENCE FROM N.A.				
STRAIN=NMRI.				
MEDLINE=22493143; PubMed=12548285;				

RESULT 14


```

DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaase; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 40.1%; Score 241; DB 13; Length 129;
Best Local Similarity 42.9%; Pred. No. 3e-20;
Matches 48; Conservative 24; Mismatches 30; Indels 10; Gaps 5;

Qy 2 NWATFQOKHLINT-PIICNTIMDNNIYVGQCKRVNTFTFISSATTVKAICTGVI-MNMV 59
Db 25 DWATFKKHLTDTWDVDCNLMPTSLF----DCKDKNTFIYSLPGPVKALCRGVIFSADV 80

Qy 60 LSTTRFQLNCTRTSITPR-PCPYSSRTETNYICVKENQYVPHFAGIGRCP 110
Db 81 LNSEFYLAEC---NVKPRKPKCKYLLKSSNRICIRCHELPHVFHAGVGICP 129

RESULT 10
Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_Taxid=8408;

RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
    catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaase; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.4%; Score 224.5; DB 13; Length 128;
Best Local Similarity 39.6%; Pred. No. 2.5e-18;
Matches 44; Conservative 20; Mismatches 38; Indels 9; Gaps 4;

Qy 2 NWATFQOKHLINT-PIICNTIMDNNIYVGQCKRVNTFTFISSATTVKAICTGVI-MNMV 59
Db 25 NWETFQKKHLTDTVDKCDAMKALF----DCKQKNTFIYARPGRVQALCKNIIVSKNV 80

Qy 60 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKENQYVPHFAGIGRCP 110
Db 81 LSTDEFYSLDCNRKTL---PCHYKLLKSSNTICITCNKLPVHFVAVBECP 128

```

```

DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 132 RC-RNASEL1 RIBONUCLEASE.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBES3 CRC64;

Query Match 61.7%; Score 371; DB 13; Length 132;
Best Local Similarity 65.5%; Pred.No. 2e-35;
Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 NWATFOOKHIINTPII-CNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 59
DB 23 NNAFKFKHITSSIDCMTIMDKAIYVGGCKKERTFIISDNVKAICSGVSPDKE 82
QY 60 LSTTRFOLNCTRTSITPRCPYSSRTETNIVCKCENQYVPHFAGIGRC 109
DB 83 LSTTSFKLNTCIRDSTPRCPYHPSPDNKIKVCKEKQLPVEHVGIGKC 132

RESULT 7
Q918V8
ID Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rap1r precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
CX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR HSSP; P22069; 1ONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT CHAIN 22 132 RC-RNASEL1 RIBONUCLEASE.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 46.0%; Score 276.5; DB 13; Length 127;
Best Local Similarity 49.1%; Pred.No. 2.1e-24;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 NWATFOOKHIINT-PIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVINNV 59
DB 25 DWLTFQKHITNTRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 80
QY 60 LSTTRFOLNCTRTSITPRCPYSSRTETNIVCKCENQYVPHFAGIGRC 109
DB 81 LTTSEFYLSDC--NVTSPCKYKUKKSTNTFCVTCENQAPVHFGVGHGHC 127

us-09-961-400-24.rspt

```

	Query Match	77.6%; Score 466.5; DB 13; Length 133;
	Best Local Similarity	76.4%; Pred. No. 1.5e-46;
	Matches	84; Conservative 13; Mismatches 12; Indels 1; Gaps 1;
QY	2 NWAIFQQKHIINTPII-CNTIMDNNIIVGGCKRVNTEFISSATTVAICTGVINNVLL 60 ::: :: :: :: :: :: :: :: :: :	
DG	24 NWAIFQEIHITTSINSCTNMNSLYVGGCKKVNFIASSATTVKGICSGVTDKKL 83 :: :: :: :: :: :: :: :: :	
QY	61 STTRPQLMTCRTIRTPRCPYSRRTETNYICVKENQYPVHFAGIGRPC 110 :: :: :: :: :: :: :: :: :	
Dg	84 SSTFOLDIDCIEFRITPRPCPSRSRETNYICVKENQYPVHFAGIGGCCP 133 :: :: :: :: :: :: :: :: :	

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:30:53 ; Search time 35.3394 Seconds

(without alignments)
982.106 Million cell updates/sec

Title: US-09-961-400-24

Perfect score: 601

Sequence: 1 SNWATFOQKHINTPIICNT.....ICVKCNQYVPVHAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	555.5	92.4	133	13	Q98SM0 rana catesb
2	482.5	80.3	132	13	Q98SM2 rana catesb
3	473.5	78.8	133	13	Q98SL9 rana catesb
4	466.5	77.6	133	13	Q98SL8 rana catesb
5	443.5	73.8	132	13	Q98SM1 rana catesb
6	371	61.7	132	13	Q9DF78 rana catesb
7	276.5	46.0	127	13	Q918V8 rana pipien
8	272.5	45.3	127	13	Q8UVX5 rana pipien
9	241	40.1	129	13	Q9DFY6 rana pipien
10	224.5	37.4	128	13	Q9DFY8 rana catesb
11	221.5	36.9	128	13	Q9DFY7 rana catesb
12	212.5	35.4	128	13	Q9DFY5 rana catesb
13	158	26.3	169	13	Q9W738 xenopus lae
14	131	21.8	170	6	Q9BEC1 tragulus ja
15	128.5	21.4	144	11	Q8OZ85 mus musculus
16	128.5	21.4	153	11	Q8OXS4 mus musculus

17 127.5 21.2 147 6 Q7YRJ6
18 126 21.0 150 11 Q8VD94
19 125.5 20.9 163 6 Q9BDC2
20 124.5 20.7 116 6 Q9TVC0
21 124 20.6 150 11 Q8VD88
22 123.5 20.5 146 6 Q861Y4
23 122.5 20.4 144 6 Q9BH14
24 122.5 20.4 146 6 Q861Y3
25 122.5 20.4 146 6 Q861Y2
26 122.5 20.4 146 6 Q861Y1
27 121.5 20.2 147 6 Q7YRJ5
28 121 20.1 146 6 Q861Y5
29 120.5 20.0 149 11 Q8K2T2
30 120.5 20.0 149 11 Q8G6G3
31 120 20.0 150 11 Q8VD92
32 116.5 19.4 152 11 Q8VD89
33 114.5 19.1 124 6 Q9SNE6
34 112.5 18.7 148 11 Q8C7E4
35 112.5 18.7 149 11 Q8VD95
36 112 18.6 134 6 Q9BDB9
37 111.5 18.6 152 11 Q8VD84
38 111.5 18.6 156 6 Q8SQ05
39 111 18.5 148 11 Q8C6G3
40 110.5 18.4 119 6 Q9TW28
41 110.5 18.4 119 6 Q9TV30
42 109.5 18.2 142 6 Q9BEC3
43 109.5 18.2 156 6 Q8SQ06
44 109 18.1 124 6 Q9BEC2
45 108.5 18.1 156 6 Q8SQ08

ALIGNMENTS

RESULT 1

Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF000074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 92.4%; Score 555.5; DB 13; Length 133;
Best Local Similarity 94.5%; Pred. No. 6e-57;
Matches 104; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 2 NNATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFIISATTVAICTGVINNVNVL 60
DB 24 NNATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFIISATTVAICTGVINNVNVL 83